

FIG. 1 Continued

ACCAGGTGCGCTACACGCTGACCATCATGGCCCAAGGACAAOGGCATCCCGCAGAAATCAGACACCACCACCTAGAGATC
CTCATCTCGATGCCAATGACAATGCACCCAGTTCTGTGGGATTTCTACAGGGTTCCATCTTTGAGGATGCTCCACC
CTCGACAGCATCTCTCCAGGTCTCTGCCACGGACCGGACTCAGGTCCCAATGGGCGTCTCTGTACACCTTCCAGGGTG
GGACCGAGCGGCGATGGGACTTCTACATCGAGCCACGTCGGGTGTGATTCCACCCAGCGCCGCTCGACCCGGAGAAAT
GTGGCCGTGTACAACTTTGGGCTCTGGCTGTGATCGGGGAGTCCCACTCCCTTAGCGGCTCGGTAGAAATCCAGGT
GACCATCTTGGACATTAATGACAATGCCCATATGTTTGAAGGACGAATCGAGCTGTTTGTGTAGGAGAAACCCAG
TGGGTCTGGTGGTGGCAAGATTCGTGCTAACGACCTGATGAAGGCCCTAATGCCAGATCATGTATCAGATTGTGAA
GGGACATGCGCATTTCTTCCAGCTGGACCTGCTCAACGGGACCTGCGTGGCATGTGTGAGCTGAGCTTTGAGGTCCG
CGCGAGTATGCTGTGTGGTGCAGGCCAGCTGGGCTCCGCTGGTGAAGCCAGCCACGGTGCACATCTCTCTGTGAC
AGAATGACAACCCGCTGTGTCTGCCGACTTCCAGATCCCTCTTCAACAATATGTACCAACAAGTCCAAAGATTTCCTC
ACCGGCGGTGATCGGCTGCATCCCGGCCATGACCCGAGCTGTTCAGACAGCTCAACTACACCTTCTGTGACGGCAACGA
GCTGCCCTGTCTGTCTGTGACCCGCTACGGGCAATGCTGAGCTCAGCCGCGACCTGACACAACACCGCCGCTGGAGG
CGCTCATGGAGGTGTCTGTGTCTGATGGCATCCACAGGCTCAGCGGCTTCTGACCCGTGCTGTCTACCATCATCAGGAC
GACATCTGACCAACAGCATCACTGTCTGCCCTGGAGAACATGTCCAGAGAAATGTTCTGTCCCGCTGTGGCTCTCT
CGTGGAGGGGGTGGCCGCGTGTCTGCCACCAAGGACGAGCTTCTGTCTTCAACGTTCAGAACGACACCGAGCTCA
GCTCAACATCTGAACGTGACCTTCTCGGCGCTGCTGCTGCGGCGCTCCCGGCCAGTTCTTCCCGTGGAGGACCTG
CAGGAGCAGATCTACCTGAATCGGACGCTGCTGACCAACATCTCCACGACGCGCTGCTGCGCTTCGACGACAACATCTG
CCTGGCGAGCGCTCGGAGAACTACATGAAGTCCGTGTGCTGCTGCGATTCGACAGCTCCCGCGCTTCTCTAGCTCCA
CCACGCTGCTCTTCCCGCCCATCCACCCCATCAACCGGCTGCGCTGCGCTGCGCGCCCGCTTCCAGCGGCTTCTGCTG
GACAGGAGATGACCTCTGCTACTCTCGACCCGTGCGGCGCAACCGCGCTGCGCGACCGCGGAGCGCGCTACACCTG
CGAGTGTCTCGAGGACTTCACTGGAGAGCACTGTGAGGTGATGCTGCGCTCAGGCGCTGTGCTCAACGGGTGTGCAAGA
ACGGGGGACCTGCTGTGAACCTGCTCATCGGCGCTTCTACTGCTGTGTCTCTTGGCGATATGAGAGGCGCTACTGT
GAGGTGACCAACAGAGCTTCCCGCCGCTTCTGCTCACTTCCCGGCTGAGACAGCGCTTCCACTTCAACATCTC
CCTCAGCTTTCGCACTCAGCAAGCAAGCGCTTCTGCTTACCAACCGCGCTTCAATGAGAAGCAAGCTTCTATGCGCC
TGGAGATGCTGGACAGCAGGTGACGCTCACTTCTGCTGACGCGAGCAACAACGAGCGTGGACCGAAGGTTCGCAAT
GGTGTGATGACGCGCGGTGGCACTCTGTGCGAGTGCAGTACTACACAAGCCCAATATGCGCCACCTGGCGCTGCGCCA
TGGGCGTTCGCGGGAAGATGGCGGTGTGACAGTGGATGTTGTGACACAACCATGCTGTGCGCTTGGAAAGGACA
TGGGAACCTACAGCTGCGCTGCCAGGGCACTCAGAGCGCTTCAAGAAATGCTGTGATCTGACCGCGCTTCTACTCTG
GGGCTGTCCCAACCTGCCAGAGACTTCCAGTGCACAAACCGGCGTGTGTGGCTGCTATGCGGAACCTGTCTAGTGA
CGCAAAATGTGACATGCGCGGATTCATGCCCAACATGCGACCGGGAGGCTGCGCTGCTCGGAGGAACCTTCTGCG
ATGGGAGCGGCTGTGAGATGGAGGCACTGTGTCAACAGGTGGAATATGTATCTGTGTGAGTGTCCACTCCGATTCGCG
GGGAAGACTGTGAGCAAGCCATGCTCACCOCGACTTTCAGCGGTGAGAGCGTGTGTCTGAGAGCGTGTGTCTGAGTGAACAT
CATCATCTCTGTGCCCTGTGACTGGGGCTCATGTTCCGGAACCGGAGGAGGACAGCGTCTGTATGAGGCGCACAGTG
GTGGGCGCACAGCTTTCGCTTCCAGATGCTGAACAACTACTTCCAGTTTGAAGTGTCCACGGCGCTCCGATGTGGAG
TCCGTGATGCTGTCCGGTTCGCGGTACCGAGCGGAGTGGCAACCTGTGATGAGCTGAGAAATGTTAAGAGGA
CGGAGATGAGACCTGCTCACCATGACCTTGGACTATGGGATGGACCAAGCAAGCCAGATATCGGGGCGATCTC
CGGGCTGACGCTAAGGAGCGTGTGTGTGCGAGGCGCTCTGAAGACAAGGTCTCGGTGCGCGCTGGATTCCGAGGCTG
ATGCAAGAGTGAAGATGGGGGCGACGCTCACCAGCTGCGCACTGACATGAACAAACGACTCAAGGTTCAGGTTGA
CCACGCTGTGATGTGAGACCCCTGTACTTGGAGCGCTGTGCCCAATAGCGGCTGCCAGGAGCGCTGGAGGACT
ACAGCTGCGCTGTGACAAAGGCTACTTGGAAATAAATGTGTGATGCTGTGACCTGAACCTTCCGAGACATGGGG
GCTGCGTGGCTGCCCGGCTGCCCGAGGGCTACGTGTGCGAGTGTGGGCGCACTACTACGCGCGCTACTGTGAGAA
CAAACTGACCTTCCGTGCCCGAGAGCTGTGTGGGGAACCGGCTGTGTGAGGCTTCCACTGTGCGCTCAGCAAGGCT
TTGATCCGACTGTAAATAGACCAACGGCGAGTGCATGCAAGGACAATTACTACAACTCTAGCCCGAGGACCTGT
CTGCCCTGCGACTGCTTCCCGCATGGCTCCACAGCGGCACTTGGACATGGCCACCGGCGAGTGTGCTGCAAGCCCG
CCTCATCGCGCGCGAGTGCACCGCTGCCACAACCGCTTGGCGAGGTACCAACGCTCGGCTGTGAAGTATCTACAATG
GCTGTCCCAAAGCATTTGAGGCGGCGATCTGGTGGCCACAGCAAGTTCGGCGAGCGGCTGCCGTGCCATGCCCTAAG
GGATCCGTGTGAATGCGGTTCGACACTGCAAGCGGGAGAGGGCTGGCTGCCCGCAGAGCTCTTAACTGTACCAACAT
TCTCTGCTGACCTCAGGCGCATGAATGAGAAGCTGAGCGCAATGAGACGAGGTGACAGCGCGCGAGGCGCTGACG
TGTGAGGCGCGCTGCCCACTGCTACACAGCACAGGCGAGCTCTTGGCAATGAGCTGCGCACCGGCTTACCACTGCTG
GCCACGCTCTTACGACGAGAGCTGGCAGCAGGGCTTGCACCTGGCAGCCACGAGGACGCGACTTTACAGAGGAGCT
CATCCACTCGGGGAGCGGCTCTGCGCCCGAGCCACAGGCGGCGCTGGAGCAGATTCAGCGGAGGAGGCGGCGACGG
CACAGCTGCTCGCGCGCTCGAGGCTACTTCAACAACTGTGACAGCAACGCTGCGCGGAGCTACCTGCGGCGCTTCTG
ATCGTACCGCCAACTGATTTCTGTGTGACATCTTTGACAGTTCAACTTACGGGAGCCAGGCTCCCGGATTCGA
CACCATCCATGAAGAGTTCCCGAGGAGCTGAGTCTCTGCTTCTTCCAGCGGACTTCTTACAGCCACTGAAGAA
AAGAAGGCGCGCTGTGAGGCGGCTGGCGGAGGACCAACCGCGAGACCAAGCGCGCGCGGCGCTGGCCAGGAGGGAG
GCCCGATCAGCAGGCGGAGGCGACACCTGATGACGCTGCGCACTTGGCGCTGCGCTGCTGTGATCATTTACCCGACCG
GGGCGCTCTGCGCGAGCGCTACCAACCGGAGCGCTGCGGCTGCGCTTACCGGCGCAATTAATACCCCGA
TGGTGAACAGCTTCTGTACAGCGAGGGCGCTGCCCTGCCAGAGCGCGCTGCGTGGAGTGTGCGCGCTGCGCGT
CTGGAGGTGAGGAGCGAACCAAGCTGTCTGCTGCTGCAACCACTCCTGCGCGTGTGGGAGCGGAGGCTGCT



FIG. 1 Continued

TGCCCCGGGCTGGAGCTCCTGTCCAGGAAACGGACACATGTGGCTGCCAGTGCAGCCACACAGCCAGCTTTGCGGTGC
TCATGGATAATCTCCAGGCGTGAGAACGGGAGGGTCCCTGCTGGAAGATTGTCACTATGCCCTGTGTCTTTGCACTG
GCAGCCCTGCTGTGGCTTCCCTCTCTGAGCTGCTGCGCATGCTGCGCTCCAACTGCACAGCATTACAAAGCACCT
CGCCGTGGCGCTCTTCTCTCAGCTGGTGTTCGTGATTGGGATCAACAGACGGAAACCGGTTTCTGTGCACAGTGG
TTGCCATCTCTCTCACTACATCTACATGAGCACCTTTGCCCTGGACCTCTGTTGGAGAGCCCTGCATGTCTACCGCATGCTG
ACCGAGGTGCGCAACATCGAACACGGGGCCCATGGGDTTCTACTACGTTCGTGGCTGGGGCATCCCGCCATTGTACAGG
ACTGGCGGTGGGCTGGACCCCAAGGCTACGGGAACCCGACTTCTGCTGGCTGTGGCTTCAAGACACCTGTATTTGA
GCTTTGCGGGGCCATCCAGCTGTATTAATCATCAACACAGTCACCTTCTGTCTATCTGCAAGGTTTCTGCCAAGG
AAGCACCATTAATATGGGAAAAAGGGATCTCTCCCTGCTGAGGACCTCATCTCTCTGCTGTCTCATCAAGCCAC
CTGGCTGCTGGGGCTGCTGGCTGTGAACCGGCTATGCACTGAGCTTTCACTACCTCTTCCGCATCTTCAGCCGCTTACAGG
GCCCCCTTCTCTCTCTTTTCCACTGCGTGTCAACAGGAGGTCCGGAAACACCTGAAGGGGCTGCTGGCGGGAGGAAG
CTGCACCTGGAGGACTCCGCCACCAACAGGGCCACCTGCTGACGGCTCCCTCACTGCAACACACCTTCCGTGACGG
GCTGACATCTCTGACACAGCTTGGGGGAGTCCACCCCTCTCTGGACAGCATCTCTAGGGATGAAGGGATCCAGAGC
TCGGCGTCTCTCTGGGCTGGTGGGGGAGCCACGAGAGGCCAGACGGTCCCTCATGCCAGGAGCTGCAAGGATCCC
CCTGGCCAGATTCCTCACTCACATAGCGAGCTGTCCCTGGAAGAGGAGGAGCTCTTACGGCTCTCACACTGCTCAG
CAGCCAGGACCATGGGTGGGAGCTGAGGAAAAATGGGACCCGCGCCAGGGGCGCCGTCACAGCACCCCCAAAGGGGAG
CTGTAGCCAAACAGCTTCCGGCCGGCTGGGCCGAGCAGAGCTGGCTGACAGTCAAGTGAAGGACCCAGCGGCAAGGCC
CGCTGAGGATGGAGACCAAGGTTCAGCTGGAGCTCCACCGGAGGAGCAGGGCAGTCACCGTGGAGAGTACCCCCGGA
CCAGGAGAGCGGGGCCAGCCAGCTTCTAGCAGCCAGCCCCAGAGCAGAGGAAGGCATCTTCAAAAATTAAGTCA
CTACCCCTCCGCGCTGACGCTGACGGAGCAGCGCTGAAGGGCCGGCTCCGGGAGAACTGGCCGACTGTGAGCAGAGC
CCACATCTCGGCGACGTCTTCCCTGGGCTCTGGCGGCCCGACTGCCCATCACAGTCAAGAGCCCTGGGAGGGAGCC
GGGCGTGAACCACTCAACGGGTGGCCATGAATGTCCGACTGGGAGCCCCAGGCCGATGCTCCGACTCTGAGAAAC
CGTGA

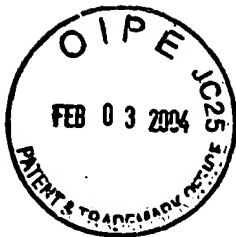


FIG. 2

M A P P P P V L F V I L L L L A A A A A L P A M G L R A A A W E P R V P G O T R A P A L R P C C T Y A V G A A C T P R A P K E L L O V G F D G R L A G R R R V S
C A C R P L P L Q V R L V A R S A P T A L S R R L R A R T H L P G C G A R A R L C G T G A R L C G A L C P P V P G C A A A Q H S A L A A P T T L P A C R C P P
R P A P C P G R P I C L P P G O S V R L R L L C A L R A A G A V A V G L A E A T A G T P S A S P S P P P L P P H L P E A R A G P A R R A R R G T S G R
G S L F P P M P S Y Q V A L F E H E P A G T L I L Q L H A R Y T I E G E E R V S Y M E G L F D E R E R O T P R I D S A T G A V S I D S V L D R E T K E T H V
L K V K A V D Y S T P P R S A T T Y I T V L V K D T H D S P V F E Q S Y R E R V R E L E V G Y E V L T R A S D R D S P I N A N L E Y R V L G G A M D V F
Q L N E S P C V V S T R A V L D R E A A E Y Q L L V E A N D O G R P G L S A T A V Y I E V E D E N D A Y P P S E Q N Y V V Q V P E D V G L N T A V L B
V O A T D R D Q G Q N A I H Y S I L S G N V A C Q F Y L H S L S G I L D V I N P L D F E D V Q K Y S L S I K A O G G R P P L I N S G C V S V Q V L D V N D
M E P I P V S S P P Q A T V L E N V P L C Y P V V H I Q A V D A D S G E N A R L H Y L V D T A S T F L G G S A G P K N E A P T P D P P P Q I H S S G M T
V C A L O R E E V E N T S P Q V K A V D E G S P P H S S T S V S I T V L V N D E S P V F T Q P T Y E L R L E D A A V G S S V L T Q A R D R A N S V I
T T Q L T G C H T R R F A L S S Q R G G C L I T L A L P L D Y E Q Q V L A V T A S D G T R S H T A H V L I N V I D A N T H R P V P Q S S H Y T V S V E R
D R F V G T S I A T L S A N D E D T G E N A R I T Y V I Q D P V P Q R I D P S G T M Y T M H L O Y E N Q V A T T L T D A Q D N G I P Q R S D T T T L B I
L I L D A N D A P Q L N D F T Q G S I P E D A P P S T S I L Q V S A T D R D S G P N O R L Y T P Q G G D G D G D F T I E P T S G V I R T O R L D R E N
V A V Y N L A L A V D R O S P T L S A S V E I Q V T L O I N D A P H P E K D E L L V E E N P V G S V V A K I R A N D P D E G P H A Q I N Y Q I V E
G E M R H P Q L D L A W C D L R A N V E L D P E V R E Y V L V Q A T S A P L V S R A T V H I L L V D Q N D P P V L E D P Q I L P M N Y V T N K S N S P P
T O V I O C I P A H D P D V S D S L E Y T P P Q G N E L R L L L L D P A T G E L Q L S R D L D N P O L E A L M E V S V S D Q I H S V T A P C T L A V T I T D
D M L T N S I T V L E R S Q E K F L S P L L A L F V E G V A A V L S T T D O V P V F V H Q N D H V S N I L N V T P S A L L P G O V R Q P P F S E D L
Q E Q I Y L N E T L A T T I S T O R V L P T D N I C L R E F C E N Y M E C V S L R P D S S A P T L S S T P V L F R P I N P I N G L R C R C P P G P T Q D V C
E T E I D L C Y S D P G A N R C A S R E G G Y T C E C P E D T G E H C E V D A R S O R C A N G V C K N G O T C V N L I G G P H C V C P P G E Y R P Y C
E V T P R S P P P Q S P V T P R G L R O R V H P T I S I L A T A Q E R N G L L Y N C R P N E K H D F I A L E I V D E Q V L T P S A G E T T T T V A P K V S
G V S D G R M H E V Q V Y T N K P N I G H L G L F H O P S G E R M A V V T D C D T T M A V R F G R D I G N Y S C A A Q G T Q T G S E K S L D L T G P I L L
G O V N L P E D F P V H N R Q F V G C M R L S V D G K N V D H A G F I A N G T R E G C A A R R U F C D G R C O N G O T C V N E N M Y L C A C F L R F G
G K N C E Q A N P H P Q L F S G E S V S W S D L N I I S V P W Y L Q L M P R T R K E D S V L M E A T S C G P T S F R L Q I L N Y L O F E V S H G P S D V S
S V M L S Q L R V T D G E N H I L L T E L K N V K E D S E M H L V T I L D Y C M D O N K A D I G G M L P G L T V R S V V G G A S E D K V S V R R G P R C C
M Q C V R N G C T P T N V A T L D G N A L K V R V K D G C D V D P C T S S P C P P N S R C H A M E D Y S C V C D R G Y L G I N C V D A C H L P C E R N O
A C V R S P G S P Q G Y V C E C P S H Y G F Y C E N K L O L P C P R O M M O N P V C G S C B A V S K O F D P D C N K T S O C C K E N Y Y K L L A Q D T C
L E C D C P P H G S H S R T C D A T G C C A C K P G V I G R Q C N R C D N P A E V T T L C E V T Y N G C P K A F E A C I N N P Q T E P G Q P A A V P C P K
Q S V G N A V R C S C E K G N L P P E L F N C T T I S F V O L R A M E K L S N E T Q V D C A R A L Q L V R A L S A T O N T G T L P G N D V A T A Y Q L L
G H V L Q H S W Q Q G V D L A A T Q D A D P H E D V I H S G S A L L A P A T R A A M E Q I Q R S E G G T A Q L L E R L E G Y T S V A R N V A R T Y L R P V V
I V T A N I L A V D I P D K F N P T G A R V F R F O T I H E Z P P R E L S S V E P A D F P R P P E R K E G P L L R P A G E R T T P O T T R P G P G T E R E
A P L S R R R R R P D A G Q F A V A L V I I T R T L O Q L L F E R Y D P D R S L R L P H R P I I N T P M V S T L V S E C A P L R P L R P V L V R F A L
L E V B E R T K P V C V P W N H S L A V G G T G G W S A R G C E L L S R N R T H V A C Q C S H T A S F A V L E D I S R R E G E V L F L K I V T T A A V S L S L
A A L L V A P V L L S L V R M L A S N L H S I H K H L A V A L P L S Q L V P V I G I N Y T E N P F L C T V V A I L L H Y I Y N S T F A W L V E S L H V Y R L

S E V R N I D T G M R F Y V V G M P I A I V T Q L A V G L D P Q C Y G N P D F C N L S L Q D T L I N S F A G F I G A V I I I N T V T S V L S A K V S C R
I H H Y Y G K G I V S L R T A F I L L L I E A I N L L G L L A V N R D A L S P H Y L F A I P S G L Q G P F V L L P H C V L N Q E V R K H L A G V L G R K
I H L E D S A T T R A T L L T R S L N C N T P P G O G P M L R T D L G B S T A S L O S I V R D E G T O K L G V S E G L V R G S H G E P D A B L M P R S C D P
P C H D S D S D S L S L D E Q S S Y A S S H S S D E D G V G A E R F O D P A R G A V H S T P E G D A V A N H V P A G H P D O S L A E S D S E D P S G K P
R L K V E T K V S V E L H R E B Q G S H R G E Y P P D Q B E G G A R L A S S Q P P B O R K O I L K H V T Y P P L T L T E Q T L K G R L R E K L A D C E Q S
P T S E R T S S L G S G G P D C A I T V E S P C R E P C H L A N G V A N H V T O S A Q A D G S D E K P



FIG. 3

Score = 939 (140.9 bits), Expect = $4.0e-81$, Sum P(3) = $4.0e-81$
Identities = 203/218 (93%), Positives = 203/218 (93%), Strand = Plus / Plus

Query: 230 CTGTAAATAGAACCAACGCTCAGTGCAT-CCAGCAGAAATTAATACAGCTCCTAGCCC 288
CTG A T A A C GGC TG C T CCA GGAGAAATTAATACAGCTCCTAGCCC
Sbjct: 38281 CTGAAGTCACAGGCTCTGCTCTGCTTTTCCA-GGAGAAATTAATACAGCTCCTAGCCC 38339

Query: 289 AGGACACCTGTCTGCTCTGCTGCTTCCCTCATGGCTCCACAGCCGCACTTGGACA 348
AGGACACCTGTCTGCTCTGCTGCTTCCCTCATGGCTCCACAGCCGCACTTGGACA
Sbjct: 38340 AGGACACCTGTCTGCTCTGCTGCTTCCCTCATGGCTCCACAGCCGCACTTGGACA 38399

Query: 349 TGCCACCGGGCAGTGTGCTGCAAGCCCGCGTCATCGGCGCCAGTGCACCCGCTGCG 408
TGCCACCGGGCAGTGTGCTGCAAGCCCGCGTCATCGGCGCCAGTGCACCCGCTGCG
Sbjct: 38400 TGCCACCGGGCAGTGTGCTGCAAGCCCGCGTCATCGGCGCCAGTGCACCCGCTGCG 38459

Query: 409 ACAACCCGTTTGCAGAGTCAACACGCTCGGCTGTGAAG 467
ACAACCCGTTTGCAGAGTCAACACGCTCGGCTGTGAAG
Sbjct: 38460 ACAACCCGTTTGCAGAGTCAACACGCTCGGCTGTGAAG 38498



FIG. 4

Score = 1000 (352.0 bits), Expect = 2.4e-98, P = 2.4e-98
Identities = 162/186 (87%), Positives = 172/186 (92%), Frame = +3

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Query:      3 YLGINCVDAChLNPCENMGACVRSFGSPQGYVCBOGFSHYQFYCHENKLLDLPCFPGWNGNP 182
              Y G  CVDAC LNPC+++ ACVRSP +P+GY CBCCP HYG YCENK+DLPCP+GWNGNP
Sbjct: 1917 YPGKCKVDACL LNPCKHVAACVRSPNPFRCYSCEOGFGHYGYCENKVDLPCKGWAGNP 1976

Query:     183 VCGPCHCAVSQGFDPDCNKTNGQCCKENYYKLLAQDTCLPCDCFPHGSHSRTCNATGQ 362
              VCGPCHCAVS+GFDPDCNKTNGQCCKENYYK AQD CLPCDCFPHGSHSR CDM TCG
Sbjct: 1977 VCGPCHCAVSQGFDPDCNKTNGQCCKENYYKPPAQDACLPCDCFPHGSHSRACDMDTGQ 2036

Query:      61 CCTGGGTGCGCTCCCCCGGCTCCCCGCAGGGCTACGTGTGCGAGTGTGCCCCCAGTCACT 120
              |||||
Sbjct: 33445 CCTGCGTGCGCTCCCCCGGCTCCCCGCAGGGCTACGTGTGCGAGTGTGGGCCAGTCACT 33504

Query:     121 ACGGCCCGTACTGTGAGAACAA 142
              |||||
Sbjct: 33505 ACGGCCCGTACTGTGAGAACAA 33526
```



FIG. 5

Score = 12924 (4549.5 bits), Expect = 0.0, P = 0.0
Identities = 2451/3034 (80%), Positives = 2677/3034 (88%)

Query: 1 MAPPPFPVLPVLLLLAAAAALPAGLRAAAWSPRVPGGTRAFALRPGCTYAVGAACTPR- 59
MAP P VLP L+LLAAAA LPA+ L AAANE RVPGG RAFAL PG +Y + TPR
Sbjct: 1 MAPSSPRVLPALVLLAAAA-LPALELGAAGWELRVPGGARAPALGPGMSYRLDTTPTRE 59
Query: 60 ---APRELLOVGRD-GRLAGRRRVSG-AGRPLFLOVRLVARSAPTALSRLRARTHLPGC 114
RE GR G AG + AGR LPLQVRLVAR APTA S LRAR + C
Sbjct: 60 LLOVSREGPAAGRRLGLGAGTLOCARLAGRLPLQVRLVARGAPTAPSLVLRARAYGARC 119
Query: 115 GARA-RICGTGRL-----CG-ALCFPVPGGCAAAQHSALAAPTTLPACRCPPRP 162
G R R GA.L G ALCFP OG AA+ S L A T PAC CPP
Sbjct: 120 GVLLLRBARGAELRSPAVRSVPGLGDALCFPAAGGGAASITSVLEAITNYPACSCPPVA 179
Query: 163 RPRCPGRPICLPGGSVRLRLCALRRAAGAVRVGLALEAATAGTPSASPSPSPLPPNL 222
C PICL PGCS LRL-CAL RAAGAV V L ++A T+GTPS SPS SP L NL
Sbjct: 180 GTCRRROPICLRPGGSAELRLVLCALGRAAGAVVVELVIA- TSGTPSSESPSVSPLL-NL 237
Query: 223 PEARAGPARRAROTSGRQSLKFPMPHYQVALFENEPAQTLLQLHAHYTIEGSEERVSY 282
+ KAG RR+RRT 8 +FP+P+YQV++ KNEPAGT +++L AH BG+ R+SY
Sbjct: 238 SQPRAGVVRRSRRTGSGSTSPQFPLPSYQVSENEPAGTAVIELRAHDFDEGDAGRLSY 297
Query: 283 YMBGLFDRSRGYFRIDSATGAVSTDVLDRETKETHVLKVKAVDYSTPPRSATTYITVL 342
ME LFDERS GYP ID+ATGAV+T LDRETK+THVL+V AVD+ +P RSA TY+TV
Sbjct: 298 QMBALFDRSRNGYFLIDAATGAVTTARSLDRETKDTHVLKVS AVD+GSPRRSAATYITVT 357
Query: 343 VKDTNDHSPVFEQSEYREVRNLEVGVEVLTIRASDRDSPINANLRYRVLOGANDVFL 402
V DTNDHSPVFEQSEYREK+RNLVGVYEVLTIRA+D D+P NAN+RYR+L GA VF++
Sbjct: 358 VSDTNDHSPVFEQSEYREVRNLEVGVEVLTIRATDGDAPENANRYRLLEGAGGVFEI 417
Query: 403 NBSGCVVSTRAVLDRKEAAYQLLVEANDQGRNPGPLSATATVYIIVEDENDNYPQFSEQ 462
+ SGVV TRAV+DRKEAAYQLLVEANDQGRNPGPLSA+ATV+I VEDENDNYPQFSE+
Sbjct: 418 DARGGVVTRAVVDRKEAAYQLLVEANDQGRNPGPLSASATVHIVVEDENDNYPQFSEK 477
Query: 463 NYVQVQFEDVGLNTAVLKVQATDRDQGNAAIHYSILSGNVAGQFYLHSLSGILDVINPL 522
YVQVQFEDV +NTAVLKVQATDRDQGNAAIHYSI+SGH+ GQFYLHSLSG LDVINPL
Sbjct: 478 RYVQVQFEDVAVNTAVLKVQATDRDQGNAAIHYSIVSGHLKQFYLHSLSGSLVINPL 537
Query: 523 DFEDVQKYSLSIKAQDQGRPFLINSQGVSVQVLDVNDNEPIFVSSPFOATVLENVFLGY 582
DFE +++Y+L IKAQDQGRPFLINSQ+VSQVLDVNDN PIFVSSPFOA VLENVFLG+
Sbjct: 538 DFEALREYTLRIKAQDQGRPFLINSQGLVSVQVLDVNDNAPIFVSSPFOAVLENVFLGH 597
Query: 583 PVVHIQAVDADSGENARLHYRLVDTASTYLCGGSAGPKNPAFTPDFFPQIHNSGMITVC 642
V+HIQAVDAD+GENARL YRLVDTAST +GG S +NPA PDFFPQIHNSGMITVC
Sbjct: 598 SVLHIQAVDADAGENARLQYRLVDTASTIVGCSVDSENPASAPDFFPQIHNSGMITVC 657
Query: 643 AELDREEVEHYSPGVEAVDHGSPFMSSTSVSITVLDVNDNDPVFTQPTYELRLNEDAAV 702
AELDREEVEHYSPGVEAVDHGSP HSSS SVSITVLDVNDNDP+FTQPTYELRLNEDAAV
Sbjct: 658 AELDREEVEHYSPGVEAVDHGSPAMSSSASVSITVLDVNDNDPHTQPVYELRLNEDAAV 717
Query: 703 GSSVLTLQARDRDANSVITYQLTGNTKRFALSSQSGGLITLALFLDYKQBQYVLAV 762
GSSVLTL+AKDRDANSVITYQLTGNTKRFALSSQ CGGLITLALFLDYKQB+QYVLAV
Sbjct: 718 GSSVLTLRARDRDANSVITYQLTGNTKRFALSSQSGGLITLALFLDYKQBQYVLAV 777
Query: 763 TASDGTASHTAHVLINVTANTRHPVQSSHYTVSVSEDRPVGTSIATLSANDEDTGENA 822
TASDGTASHTA V INVTANTRHPVQSSHYTVSVSEDRPVGTSIAT+SA DEDTGENA
Sbjct: 778 TASDGTASHTAQVFINVTANTRHPVQSSHYTVSVSEDRPVGTSIATISATDEDTGENA 837
Query: 823 RITYVTQDPVQFRIDPDGOTMYTMDLDYEMQVAYTLTMAQNGIPQKSDTTLBILI 882
RITYV++DFVQFRIDPD+GT+YTM ELDYE+Q AYTL I AQNGIPQKSDT+LEILI
Sbjct: 838 RITYVLEDFVQFRIDPDGTITMYTMDLDYEDQAAYTLTMAQNGIPQKSDTTLBILI 897



FIG. 5 Continued

Query: 883 LDANDNAPQFLNDFYQGSIFEDAPPSTSILOVSATDRDSCGPNRLLYTFQGGDDGDDFY 942
LDANDNAP+FL DFPQGS+PEDAPPSTS+LQVSATDRDSCGPNRLLYTFQGGDDGDDFY
Sbjct: 898 LDANDNAPFLRDFYQGSVPEDAPPSTSVLQVSATDRDSCGPNRLLYTFQGGDDGDDFY 957

Query: 943 IEPTSGVIRTQRRLDRENVAVYNLWALAVDRGSPPLSASVEIQVTILDINDNAPMFKD 1002
IEPTSGVIRTQRRLDRENVAVYNLWALAVDRGSP PLSASV IQV++LDINDN P+YKCD
Sbjct: 958 IEPTSGVIRTQRRLDRENVAVYNLWALAVDRGSPNPLSASVGIQVSVLDINDNPFVFKD 1017

Query: 1003 ELLEFVEENFPVGSVVAKIRANDPDEGPNQAQIYQIVEGDMRHFQOLDLNGDLRAMVEL 1062
ELLEFVEEN+PVGSVVA+IRANDPDEGPNQAQI+YQIVEG++ FQLELL+GDLRA+VEL
Sbjct: 1018 ELLEFVEENFPVGSVVAKIRANDPDEGPNQAQIYQIVEGDMRHFQOLDLNGDLRAMVEL 1077

Query: 1063 DFEVRREYVLVVOATSAFLVSRATVHILLVDQNDNPFVLPDFQILFNNYVTHKNSNFP+G 1122
DFEVR+Y+LVVOATSAFLVSRATVHI L+QNDNPF LPDFQILFNNYVTHKNSNFP+G
Sbjct: 1078 DFEVRDYMLVVOATSAFLVSRATVHILLVDQNDNPFVLPDFQILFNNYVTHKNSNFP+G 1137

Query: 1123 VIGCIPANDPDVSDSLNYTFVQGNELRLLLLDPATGELQLSRDLDRNPLEALNEVSVD 1182
VIG IPANDPD+SDSLNYTF+QGNEL LLLDPATGELQLSRDLDRNPLEALNEVSVD
Sbjct: 1138 VIGRIPANDPDVSDSLNYTFVQGNELRLLLLDPATGELQLSRDLDRNPLEALNEVSVD 1197

Query: 1183 GHSVTAFCITLKVTTITDMLTNSITVLEEMSQKFLSPILLALFVEGVAANVLSTTKDDV 1242
GHSVTA CTLAVTTITDMLTNSITVLEEMSQKFLSPILL+LFVEGVA VLSTTKDD+
Sbjct: 1198 GHSVTALCTLKVTTITDMLTNSITVLEEMSQKFLSPILLALFVEGVAANVLSTTKDDI 1257

Query: 1243 FVFNVQNDTDVSSNMLSVTFSSALLPGGVROQFPFSEDLOEQIYLNRTLLTTISTORVLPF 1302
FVFNV+QNDTDVSSNMLSVTFSSALLPGG RQ+FPFSEDLOEQIYLNRTLLTTIS QRVLPF
Sbjct: 1258 FVFNIQNDTDVSSNMLSVTFSSALLPGGTRGRFPFSEDLOEQIYLNRTLLTTISQRVLPF 1317

Query: 1303 DNNICLREPCENYMKCVSVLRFDSSAPFLSSTTVLFRPIHPINGLRCRCPPGFTGDCYET 1362
DNNICLREPCENYMKCVSVLRFDSSAPF+SSTTVLFRPIHPI GLRCRCPPGFTGDCYET
Sbjct: 1318 DNNICLREPCENYMKCVSVLRFDSSAPFLSSTTVLFRPIHPITGLRCRCPPGFTGDCYET 1377

Query: 1363 EIDLCTYEDPCGANGRCRSEGGYTCBCFEDFTGHECEVDARSGBRCANGVCKNGGTCVNL 1422
EIDLCTYS+PCGANGRCRSEGGYTCBCFEDFTGHEC+V+ RSCRC+GVCKNGGTCVNL
Sbjct: 1378 EIDLCTYENPCGANGRCRSEGGYTCBCFEDFTGHECQVNVRSGBRCANGVCKNGGTCVNL 1437

Query: 1423 IGGPHCVCPFGYERPYCEVSTRSFPFQSFVTFRGLRQRFHPTISLFPATQERNGLLLYN 1482
IGGPHCVCPFGYER PYCEV+TRSFQSFVTFRGLRQRFHPT+SL FATQ+RN LLLYN
Sbjct: 1438 IGGPHCVCPFGYERPYCEVSTRSFPFQSFVTFRGLRQRFHPTVELAFATQERNGLLLYN 1497

Query: 1483 GRFNEKHDFIALETVDSQVQLTFSAGETTTTVAKVPVSGVSDGRNHSVQVQYNNKPNIGH 1542
GRFNEKHDFIALETV+EQ+QLTFSAGETTTT V P+VP CVSDGRNHSV VQYNNKPNIGH
Sbjct: 1498 GRFNEKHDFIALETVDSQVQLTFSAGETTTTVPQVSGVSDGRNHSVQVQYNNKPNIGH 1557

Query: 1543 LGLPHGPGSEKMAVVTVDCCDTMAVRFGKDIGNYSCAAQGTQTSKKSLLDTGPIILGG 1602
LGLPHGPGSEK+AVVTVDCCD +AV FG +GNYSCAAQGTQ+GSKKSLLDTGPIILGG
Sbjct: 1558 LGLPHGPGSEKMAVVTVDCCDAAVAVHFGSYVCNYSCAAQGTQSGSKKSLLDTGPIILGG 1617

Query: 1603 VFNLPEDFPVHNRQFVGCNRLSVDCNVDMAAFIANGTRECCEARRNFCDDRCCQNGG 1662
VFNLPEDFPVH+RQFVGCNRLS+DG+ VDMA FIANGTRECCEARRNFCDDRCCQNGG
Sbjct: 1618 VFNLPEDFPVHNRQFVGCNRLSIDGRIVDMAAFIANGTRECCEARRNFCDDRCCQNGG 1677

Query: 1663 TCVNRNMYLCECPLRFGGKNCQAMPHQPLFSGESVVSNDLNIISVFNILGLMFRTR 1722
TCVNRNMYLCECPLRFGGKNCQAMPHQ P+GESVVSNDL+I ISVFNILGLMFRTR
Sbjct: 1678 TCVNRNMYLCECPLRFGGKNCQAMPHQPLFSGESVVSNDLNIISVFNILGLMFRTR 1737



FIG. 5 Continued

Query: 2563 VRNIDTGMRFYFVVGWGIPTAVTGLAVGLDPQGTGNPDPFWLSLQDTLINSFAGPIGAV 2622
VRNIDTGMRFYFVVGWGIPTAVTGLAVGLDPQGTGNPDPFWLSLQDTLINSFAGP+G V
Sbjct: 2578 VRNIDTGMRFYFVVGWGIPTAVTGLAVGLDPQGTGNPDPFWLSLQDTLINSFAGPVQTV 2637

Query: 2623 IIINTVTSVLSAKVSCQRKHYYGKKGIVSLRTAFLLLLLISATWLLGLLAVNRDALSF 2682
IIINTV VLSAKVSCQRKHYY +KG+VE+LRTAFLLLLL++ATWLLGLLAVN D LSF
Sbjct: 2638 IIINTVIFVLSAKVSCQRKHYYERKGVVSMRTAFLLLLLVATWLLGLLAVNSDTLSF 2697

Query: 2683 HYLFAIPSCLOGPFFVLLPHCVLNQEVKHLKGVLCGRKHLKLEDSATTRATLLTRSLNCF 2742
HYLFA FS LQC FVLLPHCV ++EVRKHL+ VL C+KL L+DSATTRATLLTRSLNCF
Sbjct: 2698 HYLFAAFSCLOGIFVLLPHCVAHREVRKHLRAVLAKKLLQDDSATTRATLLTRSLNCF 2757

Query: 2743 TFGCGPMLRTDLGESTASLDSIVRDEGIQKLGVSGLVRSQSHQEPDASLMFRSCKDPPG 2802
T+ +GPDMLRT LGESTASLDS RDEG+QKL VS9G RG+HGEFD S +PR+ K C
Sbjct: 2758 TYSEGPMMLRTALGESTASLDSITRDEGVQKLVESGPARCNHGEFDTSFIPRSEKKAHG 2817

Query: 2803 HDSDSSELSLDEQSSSYASSHSSDSSEDDGVGAREKNDPARGAVHSTPAGDAVANHVPAG 2862
DESDSELSLDE 66SYASSH+SDSEDDG AE+KM+PA G HSTPK DA+ANHVPAG
Sbjct: 2818 PDSDESELSLDEHSSSYASSHTSDSEDDGGAEDKMPAGGPAHSTPKADALANHVPAG 2877

Query: 2863 WPDQSLAESDSEDPGKPKLVETKVSVELHREKQSHRGYTPDQESGGAAR---LASS 2919
WPD+SLA SDSE+ +P LKVETKVSVELHR+ QG+H G+ P D ESG A+ + SS
Sbjct: 2878 WPDSELAGSDSEKELDTFPHLVETKVSVELHRQAQGNHCGDRPSDPESGVLAKPVAVLSS 2937

Query: 2920 QPPEQRKGLKMKVITYPPFLTLTBTQTLKGLREKLADCEQSPTSSRTSSLGSG----GPD 2975
QP EQKQKGLKMKVITYPPFL EQ LK RLREKLADCEQSPTSSRTSSLGSG D
Sbjct: 2938 QPQEQKGLKMKVITYPPFLP--EQPLKSLREKLADCEQSPTSSRTSSLGSGDGVHATD 2995

Query: 2976 CAITVKEPGRFGRHNGVAMNVRTGSAQADGSDSEKP 3014
C-IT+K+P-REPGR+HLNGVAMNVRTGSAQA+GSDSEKP
Sbjct: 2996 CVITIKTPRREPGRHNGVAMNVRTGSAQANGSDSEKP 3034

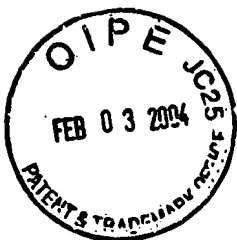


FIG. 8

MEFVRAIWGLALALGPGSAGGHPOFCGYLARLGGSVRLGALLPRAPLARARARAALARAALAPRLPH
NLSLELVVAAPPARDPASLTRGLCQALVPPGVAALLAFPEARPELLQLEHFLAAATETPVLISLRREBARAP
LGAPNPFHLQLEHWASPLETLIDVLYAVLQAHAWEDVGLALCKTQDPGCLVALWTSRAGEPPQLVLDLS
RRDTGDAGLEARLAPMAAFVGGEAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTPLFPKALPTAGLP
POLLALGEVARPPLAAIHDIQVVARALQSAAQVQPKRALLPAPVNCDDLQAGFESPGRFLARFLANT
SPQGRTPGVVWVTQSSPDEDGQCPAGQLCLDPGTNDSATLDALPAALANGSAPRALRKCCYGYCIDLER
LAEDTFFDFELYLVGDOKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTSPFTSTSLGI
MVRARDTASPIGAFMWPLHWSTWLGVPAAHLTALFLTVYEWBSPYGLTPRGNRSTVFSYSSALNLC
YAILFRRTVSSETPKCPTRILLMNLWAFCLLVLSSTANLAAVMVGDKTPEELSGHDPKGRFOTVWE
SEABAYDKSFPDMHAHMRHSAPTTPROVAMLTSDFPKLNAFMDKSLLDYEVSIDADCKLLTVGKPF
AIBGYGGLPQNSPLTSLNLSFISRYESSGFIDLHDKWYEMVPCGKRVPAVTEILOMSTYHFAGLFVLLC
LGLGSALLSSLGEHAFFRLALPRIRKOSRLQYWLHTSQKIHREALNTEPPEOSKEETAAEAEPSCPEVEQQQQ
QDQPTAPEGWKRARRAVDKERRYRFLLEPAVVVAPEADAEABAAPREGFVWLCYGRPPAARFTGAP
QFGELEERIEVARHRLQALVRRGQLLAQLGDSARHFRRLQARAAPAEAPHSGRPGSQE

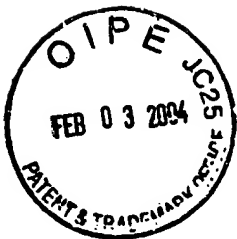


FIG. 9

Score = 3832 (575.0 bits), Expect = 0.0, Sum P(S) = 0.0
Identities = 928/1076 (86%), Positives = 928/1076 (86%), Strand = Plus / Plus

Query: 788 CACTGCCGCCCAAGCCCTGCCACCGCGGGCTGCCACCAGGCTGCTGGCGCTGGGCG 847
C CTGCC CC A G CCTG CCA C CG CT CCA GC C GGC C G G G
Sbjct: 22736 CCGTCCC-CCTAGGTTCTGCGCCACACGTC-CTTCCAGGCGCGCA-CGGGCCCCGGTGTG 22792

Query: 848 AGGTGGCAGC-ACCCCGCTGC-AGGCC-G-C-CATC-CATGACATTGTGCAACTGGTGC 901
GGTG CA G A C CC C GG A C G C C C C T A TGTG A C T G
Sbjct: 22793 -GGTGACAGGCAGCTCC-CAGGTACACATGTCTCGGCACTTTAAGGTGTGGAGCT-TGG 22849

Query: 902 CCGGGGCGCT-GGGCAGTGGCGGCCAGGTGCAGCGGAGCGAGCCCTCTCCCGGCCCG 960
CC GG C C GGG G C G CC GG CA C G G AGC C C GCG G
Sbjct: 22850 CCGGACCCACGGGCGGCTCCGGGCTGGGCCA-CGGTGGGCACTGCGCGGACGGCCA-G 22907

Query: 961 GTCAACTGCGGGACCTGCAGCCGCGCGCGCGCGAGTCCCCGGGGCG-CTTCTTGGCAG 1019
T ACT GG ACC G AG G C GC CG G CCGG C C TG C G
Sbjct: 22908 CTGGACTT--GGACCGGGAGGTGCTCTGCACG-GCCCCCGCCCCACAGGGTGGCCAG 22964

Query: 1020 GTTCTGCGCC-AA-CA-CGTCTTCCAGGCCGACACGGC-CCCCGTGGGTGACAGCA 1075
GT CTGGCC AA C CGT T A GC G G C CCC T TG GT G C
Sbjct: 22965 GT-CTGGCCCAAGCTGCGTG-TGGTAACGCTGTTGGAACACCCATTGTGTGT--GCCC 23019

Query: 1076 GCTCCCGAGAGCAAGACGGGCAUTGCCACCGGGGCACTGTGCTGGACCCCTGGCACCA 1135
G CCAGACGAGACGGGCACTGCCACGGGGCACTGTGCTGGACCCCTGGCACCA
Sbjct: 23020 GTGATCCAGAGCAAGACGGGCACTGCCACCGGGGCACTGTGCTGGACCCCTGGCACCA 23079

Query: 1136 ACCTACTCGGCCACCCCTGGACCGCACTGTTCGCGCGCTGCGCCACCGCTCAGCCCCCGTG 1195
ACGACTCGGCCACCCCTGGACCGCACTGTTCGCGCGCTGCGCCACCGCTCAGCCCCCGTG
Sbjct: 23080 ACGACTCGGCCACCCCTGGACCGCACTGTTCGCGCGCTGCGCCACCGCTCAGCCCCCGTG 23139

Query: 1196 CCTGCGCAAGTGTCTTACCGCTACTGCACTTGAACCTGCTGGAGCGCTGGCGGAGGACA 1255
CCTGCGCAAGTGTCTTACCGCTACTGCACTTGAACCTGCTGGAGCGCTGGCGGAGGACA
Sbjct: 23140 CCTGCGCAAGTGTCTTACCGCTACTGCACTTGAACCTGCTGGAGCGCTGGCGGAGGACA 23199

Query: 1256 CGCCCTTGGACTTGGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG 1315
CGCCCTTGGACTTGGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG
Sbjct: 23200 CGCCCTTGGACTTGGAGCTGTACCTCGTGGGTGACGGCAAGTACGGCGCCCTGCGGGACG 23259

Query: 1316 CCGCTGCAACCGGCTGTCTCGGCACTGCTGCGCGCGCGCGCGCCACATGGCGGTACCA 1375
GCGCTGCAACCGGCTGTCTCGGCACTGCTGCGCGCGCGCGCGCCACATGGCGGTACCA
Sbjct: 23260 GCGCTGCAACCGGCTGTCTCGGCACTGCTGCGCGCGCGCGCGCCACATGGCGGTACCA 23319

Query: 1376 GCTTCAGTATCAACTCGCGCGCTCAGAGGTGGTGGACTTCACAGCCCTTCTTCTCCA 1435
GCTTCAGTATCAACTCGCGCGCTCAGAGGTGGTGGACTTCACAGCCCTTCTTCTCCA
Sbjct: 23320 GCTTCAGTATCAACTCGCGCGCTCAGAGGTGGTGGACTTCACAGCCCTTCTTCTCCA 23379

Query: 1436 CCACCCCTCGGCATCTGTGGTGGGGCACGGGACAGCGGCTCAGCCATCGGTGCTTTATGT 1495
CCAGCCCTGGGCATCTGTGGTGGGGCACGGGACAGCGGCTCAGCCATCGGTGCTTTATGT
Sbjct: 23380 CCAGCCCTGGGCATCTGTGGTGGGGCACGGGACAGCGGCTCAGCCATCGGTGCTTTATGT 23439

Query: 1496 GCGCCCTGCACTGTGTCCAGGTGGCTGGGCGTCTTTGCGCGCTGCACTCAGCGGCTCT 1555
GCGCCCTGCACTGTGTCCAGGTGGCTGGGCGTCTTTGCGCGCTGCACTCAGCGGCTCT

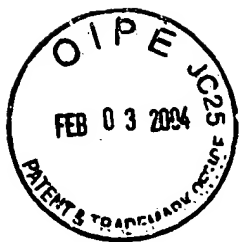


FIG. 9 Continued

Sbjct: 23440 GGGCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGGGGCCCTGCACCTCAACGGCGCTCT 23499

Query: 1556 TCCTCACCGGTGTACGAGTGGCGTAGCCCCCTACGGCCCTCACGGCACGTGGCCGCACCCCA 1615
TCCTCACCGGTGTACGAGTGGCGTAGCCCCCTACGGCCCTCACGGCACGTGGCCGCACCCCA

Sbjct: 23500 TCCTCACCGGTGTACGAGTGGCGTAGCCCCCTACGGCCCTCACGGCACGTGGCCGCACCCCA 23559

Query: 1616 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGGCATCCTCTTCAGACGCA 1675
GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGGCATCCTCTTCAGACGCA

Sbjct: 23560 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGGCATCCTCTTCAGACGCA 23619

Query: 1676 CCGTGTCCAGCAAGACGCCCAAGTGGCCACGGGCCCGCTGCTCATGAACCTCTGGGCCA 1735
CCGTGTCCAGCAAGACGCCCAAGTGGCCACGGGCCCGCTGCTCATGAACCTCTGGGCCA

Sbjct: 23620 CCGTGTCCAGCAAGACGCCCAAGTGGCCACGGGCCCGCTGCTCATGAACCTCTGGGCCA 23679

Query: 1736 TCTTCTGCCCTGCTGGTGTCTGTCCAGCTACACGGCCCAACCTGGCTGCCGTTCATGCTCGGG 1795
TCTTCTGCCCTGCTGGTGTCTGTCCAGCTACACGGCCCAACCTGGCTGCCGTTCATGCTCGGG

Sbjct: 23680 TCTTCTGCCCTGCTGGTGTCTGTCCAGCTACACGGCCCAACCTGGCTGCCGTTCATGCTCGGG 23739

Query: 1796 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGGGCTTCGGCTTCGGCACCG 1855
ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGG C GC TCGG

Sbjct: 23740 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGGTGGGCGGCTTCGGCGGC 23799

Query: 1856 TGTGGAG 1863
TG GGG G

Sbjct: 23800 TGGGGTG 23807



FIG. 10

Score = 2426 (854.0 bits), Expect = 0.0, Sum P(2) = 0.0

Identities = 463/474 (97%), Positives = 464/474 (97%), Frames = +1

Query: 1063 WVTGSSFDGQCPAGQLCLDPGTND SATLDALFAALANGSAPFALRRCCTGYCIDLLER 1242
+V FDEDGQCPAGQLCLDPGTND SATLDALFAALANGSAPFALRRCCTGYCIDLLER
Sbjct: 427 FVTANDPDEDGQCPAGQLCLDPGTND SATLDALFAALANGSAPFALRRCCTGYCIDLLER 486

Query: 1243 LAEDTFPFD FELYLVGDGKYCALRDGRWTLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 1422
LAEDTFPFD FELYLVGDGKYCALRDGRWTLVGDLLAGRAHMAVTSFSINSARSQVVDFTS
Sbjct: 487 LAEDTFPFD FELYLVGDGKYCALRDGRWTLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 546

Query: 1423 PFFSTSLGINVRARDTASPIGAFMPLHNSWLGVPFALHLTALFLTVYENRSFYGLTFR 1602
PFFSTSLGINVRARDTASPIGAFMPLHNSWLGVPFALHLTALFLTVYENRSFYGLTFR
Sbjct: 547 PFFSTSLGINVRARDTASPIGAFMPLHNSWLGVPFALHLTALFLTVYENRSFYGLTFR 606

Query: 1603 GNRSTVFSYSSALNLCYAILPRTVSSKTPKCTPGRLLMNLNAIFCLLVLSSTYANLAA 1782
GNRSTVFSYSSALNLCYAILPRTVSSKTPKCTPGRLLMNLNAIFCLLVLSSTYANLAA
Sbjct: 607 GNRSTVFSYSSALNLCYAILPRTVSSKTPKCTPGRLLMNLNAIFCLLVLSSTYANLAA 666

Query: 1783 VMVGDKTFEELSGIHDPK-----CFRPGTVWESSAEAYIKKSFPMHMHMRHSAPTFP 1944
VMVGDKTFEELSGIHDPK CFRPGTVWESSAEAYIKKSFPMHMHMRHSAPTFP
Sbjct: 667 VMVGDKTFEELSGIHDPK LHPAQCPRPGTVWESSAEAYIKKSFPMHMHMRHSAPTFP 726

Query: 1945 RGVANLTSDFPKLNAPIMDKSLLDYEVSIDADCKLLTVGKPPAIBGYGIGLPQNSPLTSN 2124
RGVANLTSDFPKLNAPIMDKSLLDYEVSIDADCKLLTVGKPPAIBGYGIGLPQNSPLTSN
Sbjct: 727 RGVANLTSDFPKLNAPIMDKSLLDYEVSIDADCKLLTVGKPPAIBGYGIGLPQNSPLTSN 786

Query: 2125 LSEFISRYKSSGFIDLLHDKWYKMPVCGKRVFAVTETLQMSIYHFAGLFVLLCLGLGSAL 2304
LSEFISRYKSSGFIDLLHDKWYKMPVCGKRVFAVTETLQMSIYHFAGLFVLLCLGLGSAL
Sbjct: 787 LSEFISRYKSSGFIDLLHDKWYKMPVCGKRVFAVTETLQMSIYHFAGLFVLLCLGLGSAL 846

Query: 2305 LSSLGSHAFFRLALPRIKGSRLQYWLHTSQKIHRAINTEPPEGSKKEETAER 2466
LSSLGSHAFFRLALPRIKGSRLQYWLHTSQKIHRAINTEPPEGSKKEETAER
Sbjct: 847 LSSLGSHAFFRLALPRIKGSRLQYWLHTSQKIHRAINTEPPEGSKKEETAER 900



FIG. 13

MEFVRALWGLALALGPGSAGGHPQCOVLARLOGSVRLGALLPRAFLARARARAALARAALAPRLPH
NLSLELVYAAPPARDPASLTRGLQCALVFPQVAALLAFPEARPELLQLHFLAAATEIPVLSLLRREARAP
LGAPNPHQLHWAASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGLVALWTSRAGRPPQLVLDLS
RRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLOCDIARARRVLEAVPPGPHWLLGTPLPKALPTAGLP
PGLLALGEVARPPLEAAIHDIYQLVARALGSAAQVQPKRALLPAPVNOGDLQAPGESPGRFLARFLANT
SFQGRTPGVVWTGSSPDEDGQCPAGQLCLDPGTINDSATLDALFAALANGSAPRALRKOCYGYCIBLER
LAEDTPDFELYLVGDKYKALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTSPFPSTSLGI
MVRARDTASPIGAPMWPLHWSTWLGVPAAHLTALFLTVYEWRSPLYGLTPRGNRSTVFSYSSALNLC
YAILFRRTVSSKTPKCTGRLLMNLWAFCLLVLSSTANLAAVMVGDKTFEELSGHDPKLEHHPAQGR
PGTVWESSABAYIKKSPDMHAHMRHSAFTTPRGVAMLTSDPPKLNAFMDKSLLDYEVSIDADCKLL
TVGKPFABEGYQGLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMPVPCGRVFAVTETLQMSIYHFAO
LFLVLLCLGLSALLSSLGHAFFRLALPRIRKGSRLQYWLHTSQKIHREALNTEPPEOSKEETABAEPSGFB
VEQQQQQDQPTAFEGWKARRAVDKERRYVRLLEPAVVVAPEADAEAAAFREGPVWLCSYGRPPA
ARPTGAPQGELOELERRIEVARERLRQALVRRGQLLAQLGDSARHRPRILLQARAAPAEAPPHSGRPGS
QB



FIG. 14

Score = 3832 (575.0 bits), Expect = 0.0, Sum P(3) = 0.0
Identities = 948/1107 (85%), Positives = 948/1107 (85%), Strand = Plus / Plus

Query: 788 CACTGCCGCCCAAGGCCCTGCCCAACGCGGGGCTGCCACCAAGGCTGCTGGCCCTGGGCG 847
C CTGCC CC A G CCTG CCA C CG CT CCA GC C GGC C G G G
Sbjct: 22736 CCTGCC-CCTAGGTTCTTGGCCAACACGTC-CTCCAGGGCCGCA-CGGGCCCGGTGTG 22792

Query: 848 AGGTGGCAGC-ACCCCGCTGG-AGGCC-G-C-CATC-CATGACATTGTGCAACTGGTGG 901
GGTG CA G A C CC C GG A C G C C C C T A TGTG A C T G
Sbjct: 22793 -GGTGACAGGCAAGCTCC-CAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCT-TCG 22849

Query: 902 CCGGGCCCT-GGCAGTGCAGCCCAAGTGCAGCCGAAGCGAGCCCTCTCCCGCCCCG 960
CC GG C C GGG G C G CC GG CA C G G AGC C C GGC G
Sbjct: 22850 CCGGACCCAGGGGCGCCCCGGCTGGGCCA-CGGTGGGCAGCTGGGGGAGGCCA-G 22907

Query: 961 GTCAACTGCCCGACCTGCAACCCGCGCGGGCCGAGTCCCGGGGGCG-CTTCTTGGCAGG 1019
T ACT GG ACC G AG G C GC CG G CCCC C C TG C G
Sbjct: 22908 CTGGACTT--GGACCGGGAGGTCCCTCTGCACG-GCCCCGCCCCACAGGGTGCOCAG 22964

Query: 1020 GTTCTGGCC-AA-CA-CGTCTTCCAGGGCCGACGGGC-CCCGTGTGGGTGACAGGCA 1075
GT CTGCC AA C COT T A GC G G C CCC T TG GT G C
Sbjct: 22965 GT--CTGGCCCAAGCTGCCTG-TGGTAACGCTGTTGGAACACCCATTGTGTTT--GCC 23019

Query: 1076 GCTCCCAAGACGAAGACGGGCACTGCCAGCGGGCAGCTGTGCCCTGACCCCTGGCACCA 1135
G CCAGACGAAGACGGGCACTGCCAGCGGGCAGCTGTGCCCTGACCCCTGGCACCA
Sbjct: 23020 GTGATCCAGACGAAGACGGGCACTGCCAGCGGGCAGCTGTGCCCTGACCCCTGGCACCA 23079

Query: 1136 ACGACTGGGCCACCTTGGACGCACTGTTGCCCGCGCTGGCCCAACGGCTCAGCGCCCCGTG 1195
ACGACTGGGCCACCTTGGACGCACTGTTGCCCGCGCTGGCCCAACGGCTCAGCGCCCCGTG
Sbjct: 23080 ACGACTGGGCCACCTTGGACGCACTGTTGCCCGCGCTGGCCCAACGGCTCAGCGCCCCGTG 23139



FIG. 14 Continued

Query: 1196 CCCTGCCCAAGTGCCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 1255
CCCTGCCCAAGTGCCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA
Sbjct: 23140 CCCTGCCCAAGTGCCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 23199

Query: 1256 CGCCCTTCGACTTCGAGCTGTACTCTGTTGGGTGACGGCAAGTACGGCGCCCTTCGGGACG 1315
CGCCCTTCGACTTCGAGCTGTACTCTGTTGGGTGACGGCAAGTACGGCGCCCTTCGGGACG
Sbjct: 23200 CGCCCTTCGACTTCGAGCTGTACTCTGTTGGGTGACGGCAAGTACGGCGCCCTTCGGGACG 23259

Query: 1315 GCGCTGGACCGCCCTGGTTCGGGGACCTGCTGGCGCGCGGCCACATGGCGGTACCA 1375
GCGCTGGACCGCCCTGGTTCGGGGACCTGCTGGCGCGCGGCCACATGGCGGTACCA
Sbjct: 23260 GCGCTGGACCGCCCTGGTTCGGGGACCTGCTGGCGCGCGGCCACATGGCGGTACCA 23319

Query: 1376 GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACCAAGCCCTTCTTCTCCA 1435
GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACCAAGCCCTTCTTCTCCA
Sbjct: 23320 GCTTCAGTATCAACTCCGCCCGCTCACAGGTGGTGGACTTCACCAAGCCCTTCTTCTCCA 23379

Query: 1436 CCAGCTTGGGCATCATGGTGGCGGCACGGGACACGGCCCTCACCCATCGGTGGCTTTATGT 1495
CCAGCTTGGGCATCATGGTGGCGGCACGGGACACGGCCCTCACCCATCGGTGGCTTTATGT
Sbjct: 23380 CCAGCTTGGGCATCATGGTGGCGGCACGGGACACGGCCCTCACCCATCGGTGGCTTTATGT 23439

Query: 1496 GGCCCTTCGACTGGTCCACGTGGCTGGCGCTCTTTGGCGCCCTGCACCTCACCGCGCTCT 1555
GGCCCTTCGACTGGTCCACGTGGCTGGCGCTCTTTGGCGCCCTGCACCTCACCGCGCTCT
Sbjct: 23440 GGCCCTTCGACTGGTCCACGTGGCTGGCGCTCTTTGGCGCCCTGCACCTCACCGCGCTCT 23499

Query: 1556 TCCTCACCGTGTACGAGTGGCGTAGCCCTACGGCCCTCACGCCACGTGGCGGCAACCGCA 1615
TCCTCACCGTGTACGAGTGGCGTAGCCCTACGGCCCTCACGCCACGTGGCGGCAACCGCA
Sbjct: 23500 TCCTCACCGTGTACGAGTGGCGTAGCCCTACGGCCCTCACGCCACGTGGCGGCAACCGCA 23559

Query: 1616 GCACCGTCTTCTCTACTCTCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGAGCA 1675
GCACCGTCTTCTCTACTCTCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGAGCA
Sbjct: 23560 GCACCGTCTTCTCTACTCTCTCAGCCCTCAACCTGTGCTACGCCATCCTCTTCAGAGCA 23619

Query: 1676 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCGGCTGCTCATGAACCTCTGGGCCA 1735
CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCGGCTGCTCATGAACCTCTGGGCCA
Sbjct: 23620 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCGGCTGCTCATGAACCTCTGGGCCA 23679

Query: 1736 TCTTCTGCTGCTGGTGTCTTCCAGCTACACGCCCAACCTGGCTGCCGTCTATGGTGGGG 1795
TCTTCTGCTGCTGGTGTCTTCCAGCTACACGCCCAACCTGGCTGCCGTCTATGGTGGGG
Sbjct: 23680 TCTTCTGCTGCTGGTGTCTTCCAGCTACACGCCCAACCTGGCTGCCGTCTATGGTGGGG 23739

Query: 1796 ACAAGACCTTCGAGGAGCTGTTCGGGATCCACGACCCCAAGCTGCACACC--CGGCGAG 1854
ACAAGACCTTCGAGGAGCTGTTCGGGATCCACGACCCCAAGCTGCACACC--CGGCGAG
Sbjct: 23740 ACAAGACCTTCGAGGAGCTGTTCGGGATCCACGACCCCAAGCTGCACACC--CGGCGAG 23796

Query: 1855 GGCTTCGGCTTCGGCACCTGTGGGAGACAGC--CCGAG 1894
GGCTTCGGCTTCGGCACCTGTGGGAGACAGC--CCGAG
Sbjct: 23797 GGCTTCGGCTTCGGCACCTGTGGGAGACAGC--CCGAG 23834

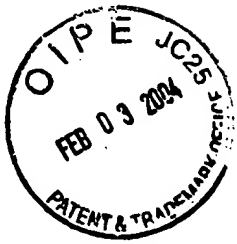


FIG. 15

Score = 2481 (873.4 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 469/474 (98%), Positives = 470/474 (99%), Frame = +1

Query: 1063 WVTGSSPEDGQCQCPAGQCLDPGTND SATLDALFAALANGSAPRALRKCCYGYCIDLLER 1242
+V PDEDQCQCPAGQCLDPGTND SATLDALFAALANGSAPRALRKCCYGYCIDLLER
Sbjct: 427 FVFARDFDEDGQCQCPAGQCLDPGTND SATLDALFAALANGSAPRALRKCCYGYCIDLLER 486

Query: 1243 LAEDTFFDFELYLVDGDKYCALRDGRNTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 1422
LAEDTFFDFELYLVDGDKYCALRDGRNTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS
Sbjct: 487 LAEDTFFDFELYLVDGDKYCALRDGRNTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 546

Query: 1423 PFFSTSLGINVRARDTASPIGAPMPLHNSWLGVPFAALHLTALFLTVYENRSPYGLTPR 1602
PFFSTSLGINVRARDTASPIGAPMPLHNSWLGVPFAALHLTALFLTVYENRSPYGLTPR
Sbjct: 547 PFFSTSLGINVRARDTASPIGAPMPLHNSWLGVPFAALHLTALFLTVYENRSPYGLTPR 606

Query: 1603 GRNRSTVFSYSSALNLCYAILFRRTVSSKTFECPTGRLMMMAIFCLLVLSSTYANLAA 1782
GRNRSTVFSYSSALNLCYAILFRRTVSSKTFECPTGRLMMMAIFCLLVLSSTYANLAA
Sbjct: 607 GRNRSTVFSYSSALNLCYAILFRRTVSSKTFECPTGRLMMMAIFCLLVLSSTYANLAA 666

Query: 1783 VMVGDKTFEELSGIHDPKLHHPAQGFRTGTVWESSAEAYIKKSFPDGAHMRHSAFTTP 1962
VMVGDKTFEELSGIHDPKLHHPAQGFRTGTVWESSAEAYIKKSFPDGAHMRHSAFTTP
Sbjct: 667 VMVGDKTFEELSGIHDPKLHHPAQGFRTGTVWESSAEAYIKKSFPDGAHMRHSAFTTP 726

Query: 1963 RGVANLTSDPPKLNAPINDKSLDYEVSIDADCKLLTVGKPPAIEGTGIGLPQNSPLTSN 2142
RGVANLTSDPPKLNAPINDKSLDYEVSIDADCKLLTVGKPPAIEGTGIGLPQNSPLTSN
Sbjct: 727 RGVANLTSDPPKLNAPINDKSLDYEVSIDADCKLLTVGKPPAIEGTGIGLPQNSPLTSN 786

Query: 2143 LSEFISRYKSSGFIDLLHDKWYKMFPCGKRVPFVAVTETLQNSIYHFAGLFVLLCLGLGSAL 2322
LSEFISRYKSSGFIDLLHDKWYKMFPCGKRVPFVAVTETLQNSIYHFAGLFVLLCLGLGSAL
Sbjct: 787 LSEFISRYKSSGFIDLLHDKWYKMFPCGKRVPFVAVTETLQNSIYHFAGLFVLLCLGLGSAL 846

Query: 2323 LSSLGEHAFPRALPRIRKGSRLQYWLHTSQKIHRAHNTPEPESKEETAERAP 2484
LSSLGEHAFPRALPRIRKGSRLQYWLHTSQKIHRAHNTPEPESKEETAERAP
Sbjct: 847 LSSLGEHAFPRALPRIRKGSRLQYWLHTSQKIHRAHNTPEPESKEETAERAP 900



FIG. 18

MEFVRALWLGLALALGPGSAAGGHFQPCGVLARLGGSVRLGAILPRAPLARARARAALARAALAPRLPH
NLSLELVVAAPPARDPASLTROLCQALVPPGVAALLAPPEARPELLQLHFLAAATETPVLSLLRRRARAP
LQAFNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGLVALWTSRAGRPPQLVLDLS
RRDTGDAGLRARLAPMAAPVOGEAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLP
PGLLALGHEVARPPLEAAHEDIVQLVARALGSAAQVQPKRALLPAPVNOGDLQAPGESPGRFLARFLANT
SFQGRGTGPVWVTGSSQVHMSRHPKVWSLRDPRGAPAWATVGSWRDOQLDLEPGGASARPPPPQGAQ
VWPKLRVVTILLEHFFVFARDPDEDGQCPAGQLCLDPOTNDSATLDALFAALANGSAPRALRKCCYGYCI
DLIERLAEDTTPDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSPSINSARSQVVDFTSPFFS
TSLGIMVRARDTASPIGAPMWPLHWSTWLGVFALHLTALFLTVYEWRSFYGLTPRGNRSTVRSYSSA
LNLGYALFRRTVSSKTPKCPTGRLLMNLWAIPCLLVLSYNTANLAAVMVGDKIFEELSGHDPKLHHPA
QGFRPGTVWESSABAYIKKSFPDMHAHMRRHSAPTTPRGVAMLTSDPPKLNAFIMDKSLLDYEVSIDAD
CKLLTVGKPPAIBGYGIGLPQNSPLTSNLSEFISRYKSSGFDLLHDKWYKMPCKGRVFAVTETLQMSY
HFAGLFVLLCLGLGSALLSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIERALNTEPPGSKHETABAEF
SGFEVEQQQQQDQPTAFEGWKARRAVDKERRVRFLEPAVVVAPEADAEAEAPREGPVWLCSYG
RPPAARPTGAPQPGELQELERRIEVARERLROALVRRGQLLAQLGDSARHRPRRLQARAAPAHAPPSG
RPGSQE



FIG. 19

Score = 5188 (778.4 bits), Expect = 0.0, Sum P(4) = 0.0
Identities = 1068/1092 (97%), Positives = 1068/1092 (97%), Strand = Plus / Plus

Query: 1019 GGTTCCTGGCCACACGTCCTTCACAGGCCGACAGGCCCGCTGTGGGTGACAGGCAGCT 1078
GGTTCCTGGCCACACGTCCTTCACAGGCCGACAGGCCCGCTGTGGGTGACAGGCAGCT
Sbjct: 22747 GGTTCCTGGCCACACGTCCTTCACAGGCCGACAGGCCCGCTGTGGGTGACAGGCAGCT 22806

Query: 1079 CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCGGGACCCACGGGGCG 1138
CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCGGGACCCACGGGGCG
Sbjct: 22807 CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCGGGACCCACGGGGCG 22866

Query: 1139 CCCCCGCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGCACCGGGAG 1198
CCCCCGCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGCACCGGGAG
Sbjct: 22867 CCCCCGCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGCACCGGGAG 22928

Query: 1199 GTGCTCTGCACGCCCCCCCCCCCCACAGGGTGCCTAGGTCTGGCCCAAGCTGCGTGTGG 1258
GTGCTCTGCACGCCCCCCCCCCCCACAGGGTGCCTAGGTCTGGCCCAAGCTGCGTGTGG
Sbjct: 22927 GTGCTCTGCACGCCCCCCCCCCCCACAGGGTGCCTAGGTCTGGCCCAAGCTGCGTGTGG 22986

Query: 1259 TAAAGCTGTTCGAACACCCATTGTGTATTGCCCGTGTATCCAGACGAAGACGGCCAGTGC 1318
TAAAGCTGTTCGAACACCCATTGTGTATTGCCCGTGTATCCAGACGAAGACGGCCAGTGC
Sbjct: 22987 TAAAGCTGTTCGAACACCCATTGTGTATTGCCCGTGTATCCAGACGAAGACGGCCAGTGC 23046

Query: 1319 CAGCGGGGCACTGTGCTTGCACCCCTGGCACCACGACTCGGCCACCCCTGGACGCACTGT 1378
CAGCGGGGCACTGTGCTTGCACCCCTGGCACCACGACTCGGCCACCCCTGGACGCACTGT
Sbjct: 23047 CAGCGGGGCACTGTGCTTGCACCCCTGGCACCACGACTCGGCCACCCCTGGACGCACTGT 23106

Query: 1379 TCGCCGGCTGGCCACGGCTCAGCGCCCCGTGCCCTGCGCAAGTCTGCTACGGCTACT 1438
TCGCCGGCTGGCCACGGCTCAGCGCCCCGTGCCCTGCGCAAGTCTGCTACGGCTACT
Sbjct: 23107 TCGCCGGCTGGCCACGGCTCAGCGCCCCGTGCCCTGCGCAAGTCTGCTACGGCTACT 23166



FIG. 19 Continued

Query: 1439 GCATTGACCTGCTGGAGCGGCTGGCGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG 1498
GCATTGACCTGCTGGAGCGGCTGGCGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG
Sbjct: 23167 GCATTGACCTGCTGGAGCGGCTGGCGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG 23226

Query: 1499 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCCTGACCGGCTTGGTGGGGGACC 1558
TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCCTGACCGGCTTGGTGGGGGACC
Sbjct: 23227 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCCTGACCGGCTTGGTGGGGGACC 23286

Query: 1559 TGTGCGCGCGCGCGCGCCACATGGCGGTACCCAGCTTCAGTATCAACTCCGCGCGCTCAC 1618
TGTGCGCGCGCGCGCGCCACATGGCGGTACCCAGCTTCAGTATCAACTCCGCGCGCTCAC
Sbjct: 23287 TGTGCGCGCGCGCGCGCCACATGGCGGTACCCAGCTTCAGTATCAACTCCGCGCGCTCAC 23346

Query: 1619 AAGTGGTGGACTTCACCAGCCCCCTTCTTCTCCACCAGCCTGGGCATCATGGTGGCGGCAC 1678
AAGTGGTGGACTTCACCAGCCCCCTTCTTCTCCACCAGCCTGGGCATCATGGTGGCGGCAC
Sbjct: 23347 AAGTGGTGGACTTCACCAGCCCCCTTCTTCTCCACCAGCCTGGGCATCATGGTGGCGGCAC 23406

Query: 1679 GGGACACGGGCTCACCCATCGGTGCTTTATGTGGCGGCTGCACCTGGTCCAGGTGGCTGG 1738
GGGACACGGGCTCACCCATCGGTGCTTTATGTGGCGGCTGCACCTGGTCCAGGTGGCTGG
Sbjct: 23407 GGGACACGGGCTCACCCATCGGTGCTTTATGTGGCGGCTGCACCTGGTCCAGGTGGCTGG 23466

Query: 1739 GCGTCTTTGCGGCGCTGCACCTCACCGGCTCTTCTCACCGTGTACAGTGGCGTAGCC 1798
GCGTCTTTGCGGCGCTGCACCTCACCGGCTCTTCTCACCGTGTACAGTGGCGTAGCC
Sbjct: 23467 GCGTCTTTGCGGCGCTGCACCTCACCGGCTCTTCTCACCGTGTACAGTGGCGTAGCC 23526

Query: 1799 CCTACGGGCTCACGCCACGTGGCGGCAACCGCAGCAGCTGTCTCTCTACTCTCTACGCC 1858
CCTACGGGCTCACGCCACGTGGCGGCAACCGCAGCAGCTGTCTCTCTACTCTCTACGCC
Sbjct: 23527 CCTACGGGCTCACGCCACGTGGCGGCAACCGCAGCAGCTGTCTCTCTACTCTCTACGCC 23586

Query: 1859 TCAACCTGTGCTACGCCATCCTCTTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC 1918
TCAACCTGTGCTACGCCATCCTCTTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC
Sbjct: 23587 TCAACCTGTGCTACGCCATCCTCTTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC 23646

Query: 1919 CCACGGGCGGCTGCTCATGAACCTCTGGGCCATCTTCTGCTGCTGGTGTCTGCTACGCT 1978
CCACGGGCGGCTGCTCATGAACCTCTGGGCCATCTTCTGCTGCTGGTGTCTGCTACGCT
Sbjct: 23647 CCACGGGCGGCTGCTCATGAACCTCTGGGCCATCTTCTGCTGCTGGTGTCTGCTACGCT 23706

Query: 1979 ACACGGCCAACTGGCTGCCGTATGGTGGGGACAAGACCTTCGAGGAGCTGTGGGGA 2038
ACACGGCCAACTGGCTGCCGTATGGTGGGGACAAGACCTTCGAGGAGCTGTGGGGA
Sbjct: 23707 ACACGGCCAACTGGCTGCCGTATGGTGGGGACAAGACCTTCGAGGAGCTGTGGGGA 23766

Query: 2039 TCCACGACCCCAAGCTGCACACC-CGGCGCAGGGCTTCGGCTTCGGCACCCTGTGGGAG 2097
TCCACGACCCCAAG T8 C CC CG 8 GGGCT C G T GGC G G GGG
Sbjct: 23767 TCCACGACCCCAAGTGGCGGGCTTCGG-G--GGGCTGGGGT--GGGCTTGGG-GGGCT 23820

Query: 2098 AGCAGCG-CGGAG 2110
AGC G G CC GG
Sbjct: 23821 AGCGGTGGCCCCGG 23834



FIG. 20

Score = 4730 (1665.0 bits), Expect = 0.0, P = 0.0
Identities = 900/900 (100%), Positives = 900/900 (100%), Frame = +1

Query: 1 HEFVRALMIGLALALGPGSAGGHPQPCGVLRLOGSVRLGALLPRAPLARARARALARA 180
HEFVRALMIGLALALGPGSAGGHPQPCGVLRLOGSVRLGALLPRAPLARARARALARA
Sbjct: 1 HEFVRALMIGLALALGPGSAGGHPQPCGVLRLOGSVRLGALLPRAPLARARARALARA 60

Query: 181 ALAPRLPHNLSLELVVAAPPARDPASL/TRGLCOALVPPGVAALLAPPEARPELLQLHFLA 360
ALAPRLPHNLSLELVVAAPPARDPASL/TRGLCOALVPPGVAALLAPPEARPELLQLHFLA
Sbjct: 61 ALAPRLPHNLSLELVVAAPPARDPASL/TRGLCOALVPPGVAALLAPPEARPELLQLHFLA 120

Query: 361 AATETPVLSLLRREARAPLGAPNPFHLQLHNASPLETLLDVLVAVLQAHAMEDVGLALCR 540
AATETPVLSLLRREARAPLGAPNPFHLQLHNASPLETLLDVLVAVLQAHAMEDVGLALCR
Sbjct: 121 AATETPVLSLLRREARAPLGAPNPFHLQLHNASPLETLLDVLVAVLQAHAMEDVGLALCR 180

Query: 541 TQDPGGLVALNTSRAGRPFQVLVDLSRDTGDAGLRARLAPMAAPVGGEAPVPAVLLGC 720
TQDPGGLVALNTSRAGRPFQVLVDLSRDTGDAGLRARLAPMAAPVGGEAPVPAVLLGC
Sbjct: 181 TQDPGGLVALNTSRAGRPFQVLVDLSRDTGDAGLRARLAPMAAPVGGEAPVPAVLLGC 240

Query: 721 DIARARKVLEAVFPGFHMLLQTFPLPKALPTACLPPCLLALGEVARPFLEAATHDIVQLV 900
DIARARKVLEAVFPGFHMLLQTFPLPKALPTACLPPCLLALGEVARPFLEAATHDIVQLV
Sbjct: 241 DIARARKVLEAVFPGFHMLLQTFPLPKALPTACLPPCLLALGEVARPFLEAATHDIVQLV 300

Query: 901 ARALGSAAGVQPKRALLPAFVNCGLQAGPESPGRTFLARFLANTSFGQRTGPPVWTGSS 1080
ARALGSAAGVQPKRALLPAFVNCGLQAGPESPGRTFLARFLANTSFGQRTGPPVWTGSS
Sbjct: 301 ARALGSAAGVQPKRALLPAFVNCGLQAGPESPGRTFLARFLANTSFGQRTGPPVWTGSS 360

Query: 1081 QVHMSRHFVWSLRDPRGAPANATVGSWEDGQLDLEFGQASARPPFPQGAQVWPKLRVV 1260
QVHMSRHFVWSLRDPRGAPANATVGSWEDGQLDLEFGQASARPPFPQGAQVWPKLRVV
Sbjct: 361 QVHMSRHFVWSLRDPRGAPANATVGSWEDGQLDLEFGQASARPPFPQGAQVWPKLRVV 420

Query: 1261 TLLSHFFVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCTGYC 1440
TLLSHFFVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCTGYC
Sbjct: 421 TLLSHFFVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCTGYC 480

Query: 1441 IDLLERLAEDTFFDFELVVGCKYGALEDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ 1620
IDLLERLAEDTFFDFELVVGCKYGALEDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ
Sbjct: 481 IDLLERLAEDTFFDFELVVGCKYGALEDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ 540



FIG. 20 Continued

Query: 1621 VVDFTSPFFSTSLGDMVRARDTASPIGAFHNFLENSTWLGVTAAALHLTALFLTVYENRSP 1800
VVDFTSPFFSTSLGDMVRARDTASPIGAFHNFLENSTWLGVTAAALHLTALFLTVYENRSP
Sbjct: 541 VVDFTSPFFSTSLGDMVRARDTASPIGAFHNFLENSTWLGVTAAALHLTALFLTVYENRSP 600

Query: 1801 YGLTPRGNRSTVFTSYSSALNLCYAILFRRTVSSKTPKCPGRLNHLNAIFCLLVLSY 1980
YGLTPRGNRSTVFTSYSSALNLCYAILFRRTVSSKTPKCPGRLNHLNAIFCLLVLSY
Sbjct: 601 YGLTPRGNRSTVFTSYSSALNLCYAILFRRTVSSKTPKCPGRLNHLNAIFCLLVLSY 660

Query: 1981 TANLAAMVVGDKTFEELSGIHDFKLHHPAQGFAPGTWESSAEAYIKKSFFDMHAMRRH 2160
TANLAAMVVGDKTFEELSGIHDFKLHHPAQGFAPGTWESSAEAYIKKSFFDMHAMRRH
Sbjct: 661 TANLAAMVVGDKTFEELSGIHDFKLHHPAQGFAPGTWESSAEAYIKKSFFDMHAMRRH 720

Query: 2161 SAPTTFRGVAMLTSDPPKLNAPIMDKSLLDYEVSIDADCKLLTVGKPPAIBGYGIGLPQN 2340
SAPTTFRGVAMLTSDPPKLNAPIMDKSLLDYEVSIDADCKLLTVGKPPAIBGYGIGLPQN
Sbjct: 721 SAPTTFRGVAMLTSDPPKLNAPIMDKSLLDYEVSIDADCKLLTVGKPPAIBGYGIGLPQN 780

Query: 2341 SPLTSHLSEFISRYKSSGFIDLLHDKWYQIVPCGRVFAVTETLQMSIYHPAGLFVLLCL 2520
SPLTSHLSEFISRYKSSGFIDLLHDKWYQIVPCGRVFAVTETLQMSIYHPAGLFVLLCL
Sbjct: 781 SPLTSHLSEFISRYKSSGFIDLLHDKWYQIVPCGRVFAVTETLQMSIYHPAGLFVLLCL 840

Query: 2521 GLGSALLSSLGERAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPGSKKESTABAP 2700
GLGSALLSSLGERAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPGSKKESTABAP
Sbjct: 841 GLGSALLSSLGERAFFRLALPRIRKGSRLQYWLHTSQKIHRALNTEPPGSKKESTABAP 900



FIG. 22

21659259_EXT_3 MEEVRAIWLGLALALGP GSAGGH PQCGVL EARLGGSVRIGALLPEA PLAKARAKAALARA
21659259_EXT_2 MEEVRAIWLGLALALGP GSAGGH PQCGVL EARLGGSVRIGALLPEA PLAKARAKAALARA
21659259_EXT_1 MEEVRAIWLGLALALGP GSAGGH PQCGVL EARLGGSVRIGALLPEA PLAKARAKAALARA
21659259_EXT_3 ALAPRLPHNLSTELVVAAPPARDPASTTRGLGQALVPPGVAAALAEFEARPELLQLHFLA
21659259_EXT_2 ALAPRLPHNLSTELVVAAPPARDPASTTRGLGQALVPPGVAAALAEFEARPELLQLHFLA
21659259_EXT_1 ALAPRLPHNLSTELVVAAPPARDPASTTRGLGQALVPPGVAAALAEFEARPELLQLHFLA
21659259_EXT_3 AATEPVLSTLRREARAPLGAPNPHLQLHWA SPLETLIDVLVAVLQAHAWEDVGLALGR
21659259_EXT_2 AATEPVLSTLRREARAPLGAPNPHLQLHWA SPLETLIDVLVAVLQAHAWEDVGLALGR
21659259_EXT_1 AATEPVLSTLRREARAPLGAPNPHLQLHWA SPLETLIDVLVAVLQAHAWEDVGLALGR
21659259_EXT_3 FODPGGLVALWTSRAGRPPQLVLDLSKRD TGDAGLRARLAPMAAPVGGEPVPAVAVLGG
21659259_EXT_2 FODPGGLVALWTSRAGRPPQLVLDLSKRD TGDAGLRARLAPMAAPVGGEPVPAVAVLGG
21659259_EXT_1 FODPGGLVALWTSRAGRPPQLVLDLSKRD TGDAGLRARLAPMAAPVGGEPVPAVAVLGG
21659259_EXT_3 DIARARRVLEAVPPGPHWLLGTPLEPKALPTAGLPPGLLALGEVARPLEAATHDIVQLV
21659259_EXT_2 DIARARRVLEAVPPGPHWLLGTPLEPKALPTAGLPPGLLALGEVARPLEAATHDIVQLV
21659259_EXT_1 DIARARRVLEAVPPGPHWLLGTPLEPKALPTAGLPPGLLALGEVARPLEAATHDIVQLV
21659259_EXT_3 ARALGSAAQVOPKRALLPAPVNGGDLQOPAGPESPGRELAREPLANTSFOGR TGPVWVTGSS
21659259_EXT_2 ARALGSAAQVOPKRALLPAPVNGGDLQOPAGPESPGRELAREPLANTSFOGR TGPVWVTGSS
21659259_EXT_1 ARALGSAAQVOPKRALLPAPVNGGDLQOPAGPESPGRELAREPLANTSFOGR TGPVWVTGSS
21659259_EXT_3 QVHMSRHFKEVWSLRKDPKCAPAWATVGSWRDQLDLBFGGASALPPPEQGAQVWPELRV
21659259_EXT_2 QVHMSRHFKEVWSLRKDPKCAPAWATVGSWRDQLDLBFGGASALPPPEQGAQVWPELRV
21659259_EXT_1 QVHMSRHFKEVWSLRKDPKCAPAWATVGSWRDQLDLBFGGASALPPPEQGAQVWPELRV
21659259_EXT_3 TLLBHPVFARDPDEDGQCPAGQGLGDPGINDSAILDALFAALANGSAPRALRKGCGYGYC
21659259_EXT_2 TLLBHPVFARDPDEDGQCPAGQGLGDPGINDSAILDALFAALANGSAPRALRKGCGYGYC
21659259_EXT_1 TLLBHPVFARDPDEDGQCPAGQGLGDPGINDSAILDALFAALANGSAPRALRKGCGYGYC



FIG. 22 Continued

21659259_EXT_3
21659259_EXT_2
21659259_EXT_1

RLLQARAAPAEAPPHSGRPGSQE
RLLQARAAPAEAPPHSGRPGSQE
RLLQARAAPAEAPPHSGRPGSQE



FIG. 23

ACGCGTTACTCCTACCAGGTTGTAGCATGCATCTTTTTGAGAGAGCAGCTGGGATCGAGTA
TACTCTTGACTTAAATATGTTTGTATAAAGACAAATGGAGAAATCAATTTTTTCCCTGA
ATTCTTAGGAGCACTTTAGTGAATAAAGAACCTGACAGTATGCTGGGCCACATGTTAAGG
ACAAAGGTGTCTGGGGAATAAGCAAGATCATAGAGGAGCTTTCTTAATTGACCGAAGTCC
TGAGTACTTCGAACCCATTTGAACTACTTGCCTCATGGACAGCTCATTGTAAATGATGGCA
TTAATTTATTGGGTGTGTTAGAAGAAGCAAGATTTTTTGGTATTGACTCATTGATGAACAC
CTAGAAGTGGCAATAAAGAATTCTCAACCACCGGAGGATCATTACCAATATCCCGAAAGG
AAATTTGTCCGATTTTTGCTAGCAACTCCAACCAAGTCAGAACTGCGATGCCAGGGTTTGAA
CTTCAGTGGTGTGATCTTTCTCGTTTGACCTTCGATACATTAACCTCAAAATGGCCAATT
TAAGCCGCTGTAATCTTGCACATGCAAATCTTTGCTGTGCAAATCTTGAACGAGCTGATCTC
TCTGGATCAGTGCTTGACTGTGCGAATCTCCAGGGAGTCAAGATGCTCTGTTCTAATGCAG
AAGGAGCATCCCTGAAACTGTGTAATTTGAGGATCCTTCTGGTCTTAAAGCCAATTTAGA
AGGTGCTAATCTGAAAGGTGTGGATATGGAAGGAAGTCAGATGACAGGAATTAACCTGAG
AGTGGCTACCTTAAAAAATGCAAAAGTTGAAGAAGTGTAACTCAGAGGAGCAACTCTGGC
AGGAACTGATTTAGAGAATTGTGATCTGTCTGGGTGTGATCTTCAAGAAGCCAACCTGAGA
GGGTCCAACGTGAAGGGAGCTATATTGAAGAGATGCTGACACCACTACACATGTACAAAA
GTGTCAGATGAGAATTTTAGGGGCTGGAGGAAGATGTAAAAGATGAAAATGTTTTCTTAT
CACTTTTCTTTCTCCACCCACTCAGTTGTCTAGAAGAAATAACACTGTAAGGAAATTTAAAA
AAAAAAA



FIG. 24

MLAHMPKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGINLLGVLEEARFFGID
SLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGLNFGADLSRLDLRYNFKMAN
LSRCNLAHANLCCANLERADLSGSVLDGANLQGVKMLCSNABGASLKLCNFEDPSGLKANLE
GANLKGVDMEGSQMTGINLRVATLKNAKLKNCNLRGATLAGTDLENCDSLGC DLQEANLRGS
NVKGAIFEEMLTPLHMSQSVR

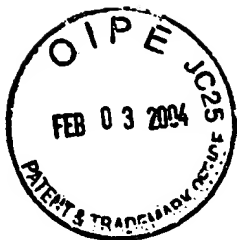


FIG. 25

Score = 1486 (523.1 bits), Expect = $1.4e-151$, P = $1.4e-151$
Identities = 286/286 (100%), Positives = 286/286 (100%), Frame
= +1

Query: 130 RSTLVNKEPDSMLAHMPKDGWGNKQDHGAPLIDRSPFYTFPIILTYLRHQQLIVHDGI 309
RSTLVNKEPDSMLAHMPKDGWGNKQDHGAPLIDRSPFYTFPIILTYLRHQQLIVHDGI
Sbjct: 104 RSTLVNKEPDSMLAHMPKDGWGNKQDHGAPLIDRSPFYTFPIILTYLRHQQLIVHDGI 163

Query: 310 NLLGVLEEARPPGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELACQGL 489
NLLGVLEEARPPGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELACQGL
Sbjct: 164 NLLGVLEEARPPGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELACQGL 223

Query: 490 NPSGADLSRLDLRYINFIQANLSRCHLAHANLCCANLERADLSGSVLDGANLQGVVHLC 669
NPSGADLSRLDLRYINFIQANLSRCHLAHANLCCANLERADLSGSVLDGANLQGVVHLC
Sbjct: 224 NPSGADLSRLDLRYINFIQANLSRCHLAHANLCCANLERADLSGSVLDGANLQGVVHLC 283

Query: 670 NAEASLKLCHNFDPSGLKANLEGANLKGVDMEGSMGTGINLEVATLKAKLQKCHLGA 849
NAEASLKLCHNFDPSGLKANLEGANLKGVDMEGSMGTGINLEVATLKAKLQKCHLGA
Sbjct: 284 NAEASLKLCHNFDPSGLKANLEGANLKGVDMEGSMGTGINLEVATLKAKLQKCHLGA 343

Query: 850 TLAGTDLENCDLSQCDLQEAHLRGSFVGAIFEEMLITPLHMSQSVR 987
TLAGTDLENCDLSQCDLQEAHLRGSFVGAIFEEMLITPLHMSQSVR
Sbjct: 344 TLAGTDLENCDLSQCDLQEAHLRGSFVGAIFEEMLITPLHMSQSVR 389

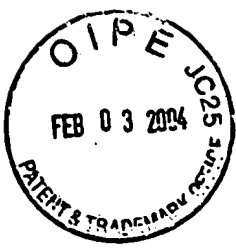
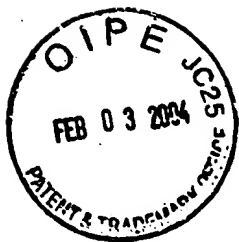


FIG. 26

TTTCCAGGGTTCTAGCCTGTTTCATCTAGCCCCATGATGGCTGTGGACATCGAGTACAGATACAACCTGCAT
GGCTCCTTCCTTGCGCCAAGAGAGGTTTTCCTTTAAGATCTCACCAAAGCCCAGCAAACCACTGAGGCCT
TGATTTCAGCTGAGCAGCAAGAATGAAGCCAGTGGAATGGTGGCCCCGGCTGTCCAGGAGAAGAAGGTGA
AAAAGCGGGTGTCTTCGCAGACAACCAGGGGCTGGCCCTGACAATGGTCAAAGTGTTCGGAATTCTGA
TGACCCGCTAGATATGCCATTCAACATCACCGAGCTCCTAGACAACATTGTGAGCTTGACGACAGCAGAG
AGCGAGAGCTTTGTTCTGGATTTTTCCAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGACTTCAGG
CCGACCACGCTGCCTTGAGAACTGTGTGCTCAAGGACAAGGCCATTGCAGGCACTGTGAAGGTTTCAGAA
CCTCGCATTTGAGAAGACCGTGAAAATAAGGATGACGTTTCGACACCTGGAAGAGCTACACAGACTTTTCCT
TGTCAGTACGTGAAGGACACTTATGCCGGTTCAGACAGGGACACGTTCTCCTTCGACATCAGCTTGCCCCG
AGAAGATTCAGTCTTATGAAAGAATGGAGTTTGCTGTGTACTACGAGTGCAATGGACAGACGTA CTGGGA
CAGCAACAGAGGCAAGA ACTATAGGATCATCCGGCTGAGTTAAATCTACCCAGGGAATGACCAAGCCC
CACAGTGGACCGGATTTGGGAATATCCTTTGACCAGTTCGGAAGCCCTCGGTGTTCTATGGTCTGTTTC
CAGAGTGGCCAAGTTACTTAGGATATGAAAAGCTAGGGCCCTACTACTA CTGACTGCAGGTGACAGGGCG
TGGCGGAGCTGCCACA



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FIG. 27

MMAVDIEYRYNCMAPSLRQERPAFKISPKPSKPLRPCIQLSSKNEASGMVAPAVQEKVKRVSFADNQG
LALTMVKVFSEFDDPLDMPFNITELLDNIVSLTTAESSEFVLDFSQPSADYLDNRRLQADHVCLENCVL
KDKALAGTVKVQNLAFKTVKIRMTFDTWKS YTDFFCQYVKDTYAGSDRDTFSFDISLPEKIQSYERMEF
AVYYECNGQTYWDSNRGKNYRIIRAEKSTQGMTKPHSGPDLGISFDQFGSPRCSYGLPPEWPSYLGYEK
LGPYY

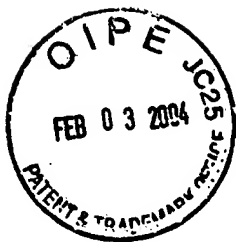


FIG. 28

Score = 3195 (479.4 bits), Expect = 2.8e-138, P = 2.8e-138
Identities = 763/903 (84%), Positives = 763/903 (84%), Strand = Plus / Plus

Query: 6 AGGGTTCTAGCCTGTTTCATCTAGCCCCATGATGGCTGTGGACATCGAGTACAGATACAAC 65
AG TTCTAGCCTG C TCTA C TGATGCG GTGGACAT GA TACAG TACA C
Sbjct: 65 AGACTTCTAGCCTGCCCCCTTAACG---TGATGGCCGTGGACATAGAATACAGCTACAGC 121

Query: 66 TGCATGGCTCCTTCTCTTGGGCCAAGAGAGGTTTGGCTTTAAGATCTCACCAAGCCGAGC 125
G ATGCG CCTC TGGC AGAG G TT CCTT AAGATCTC CC AA C A C
Sbjct: 122 AGTATGGCCCCCTTCTCTGCGCAGAGAAGCGCTTCACCTTCAAGATCTCCCCCAACTGAAC 181

Query: 126 AAACCACTGAGGCTTGTATTTCAGCTGAGCAGCAAGAATGAAGCCAGTGGAAATGGTGGCC 185
AA CCACTGAGGCTTGTATTTCAGCTG CAGCAG ATGAAGCC G GAATGGTGGCC
Sbjct: 182 AAGCCACTGAGGCTTGTATTTCAGCTGGGCAGCAAGGATGAAGCCGAGAAATGGTGGCC 241

Query: 186 CCGGCTGTCCAGGAGAAGAAGGTGAAAAAGCGGGTGTCTTCCAGACAACCGGGGCTG 245
CC C GT CAGGAGAGAAGGTGAA AAGCGGGTGTCTTCCG GACAACCGGGGCTG
Sbjct: 242 CCCACAGTACAGGAGAAGAAGGTGAAGAAGCGGGTGTCTTCCGCGACAACCGGGGCTG 301

Query: 246 GCCCTGACAATGGTCAAGTGTCTCGGAATTCGATGACCCCTAGATATGCCATTCAAC 305
GCCCT ACAATGGT AAGTGTCTCGGAATTCGATGACCC CTAGATAT CC TT AAC
Sbjct: 302 GCCCTACAATGGTGAAGTGTCTCGGAATTCGATGACCCCTAGATATTCGGTTTAAAC 361

Query: 306 ATCACCGAGCTCCTAGACAACATTGTGAGCTTGACGACAGCAGAGAGCGAGAGCTTTGTT 365
ATCAC GAGCTCCTAGACAACAT GTGAG TGACGACAGCAGAGAG GAGAGCTTTGTT
Sbjct: 362 ATCACTGAGCTCCTAGACAACATGTGAGCTTGACGACAGCAGAGAGTGAGAGCTTTGTT 421

Query: 366 CTGGATTTTCCCGAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGACTTCAGCCCGAC 425
TGGATTTT C CAGCC TCTGCAGATTACTTAGACTTTAGAAATCG CTTCAG CC AC
Sbjct: 422 TCGATTTTCCCGAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGGCTTCAGACCAAC 481

Query: 426 CACGTCTGCTTGAGAACTGTGTCTCAAGGACAAGGCCATTGCAAGCACTGTGAAGGTT 485
CA GTCTGCTT GA AACTG GTGCT AAGGA AA GCCAT CC GGCAC GT AAGGT
Sbjct: 482 CATGTCTGCTTGAAGAACTGCGTGTCTGAAGGAGAAGGCCATGCGGGCACCGTCAAGGTC 541

Query: 486 CAGAACCTGCCATTTGAGAAGACCGTGAATAAAGATGACGTTCCGACCTCGAAGAGC 545
CAGAACCT GCATT GAGAAG GTGAA AT AG ATGAC TTGGA ACCTGGAAG AGC
Sbjct: 542 CAGAACCTGCCATTGAGAAGGTTGTGAAGATCAACATGACATTTCGATACCTGGAAGAGC 601

Query: 546 TACACAGACTTTCTTGTGAGTACGTTGAAGGACACTTATGCCGTTTCAGACAGGACAGC 605
T CACAGACTT CCTTGTCACTA GTGAAGGACACTTA GC GGTTCAGACAGGACAC
Sbjct: 602 TTCACAGACTTTCTTGTGAGTATGTGAAGGACACTTACGCTGTTTCAGACAGGACACA 661

Query: 606 TTCTCCTTGGACATCAGCTTCCCGAGAAGATTCACTCTTATGAAGAATGGAGTTTCTCT 665
TTCTCCTT GA ATCAGC T CC GAGAA AT CAGTCTTATGAAGAATGGAGTT CC
Sbjct: 662 TTCTCCTTGTATATCAGCTTACCGGAGAAATCCAGTCTTATGAAGAATGGAGTTCCGC 721

Query: 666 GTGTACTACGAGTGAATGGACAGAGCTACTGGGACAGCAACAGAGGCAAGAACTATAGG 725
GTGT CTACGAGTG AA GG CAG CGTACTGGGACAGCAACA AGGCAA AACTA AGG
Sbjct: 722 GTGTCTACGAGTGAACGGCCAGTGTACTGGGACAGCAACAAGGCAAAACTACAGG 781

Query: 726 ATCATCCGGGCTGAGTTAAATCTACCCAGGGGATGACCAAGCCCCACAGTGGACCGGAT 785
ATCA C GGGC GA T A ATC ACCCAGGGGATGAC AGCC ACA TGG CCGAT
Sbjct: 782 ATCACCAGGGCCGAACCTCAGATCCACCCAGGGGATGACTGAGCCGTACAATGGCCCGAT 841

Query: 786 TTGGGAATATCCTTTGACCAGTTGGAAGCCCTGGGTGTCTCTATGGTCTGTTTCCAGAG 845
TT GGAAT TC TTGACCAGTTGG AGCCCTGGGTGTCTCT GG CTGTTTCCAGAG
Sbjct: 842 TTGGAATCTCTTTGACCAGTTGGAAGCCCTGGGTGTCTCTGAGCTGTTTCCAGAG 901

Query: 846 TGGCCAAGTTACTTAGGATATGAAAAGCTAGGGCCCTACTACTAGTGA-----CTGCAGG 900
TGGCC AGTAA T GG TATGAAAAGCT GGGCCCTA TACTAGTGA CTGCAG
Sbjct: 902 TGGCCTAGTTATCTGGGGTATGAAAAGCTGGGGCCCTATTACTAGTGAAGTTGACTGCAAT 961

Query: 901 TGACAG 906
TGACAG
Sbjct: 962 TGACAG 967



FIG. 29

Score = 1366 (480.9 bits), Expect = $1.3e-139$, P = $1.3e-139$
Identities = 255/284 (89%), Positives = 270/284 (95%)

Query: 2 MAVDIEYRYNCHAPSLRQERPAFKISPKPSKPLRPCIQLSSKNEASGMVAPAVQEKVK 61
MAVDIEY Y+ MAPSLR+ERF FKISPK +KPLRPCIQL SK+EA MVAP VQEKVK
Sbjct: 1 MAVDIEYSYSSMAPSLRERPTFKISPKLNKPLRPCIQLGSKDEAGRMVAPTQEKVK 60

Query: 62 RVSFADNQGLALTMVKVFSEFDDPLDMPFNITELLDNIVSLTTAESESFVLDFSQPSADY 121
RVSFADNQGLALTMVKVFSEFDDPLD+PFNITELLDNIVSLTTAESESFVLDF QPSADY
Sbjct: 61 RVSFADNQGLALTMVKVFSEFDDPLDIPFNITELLDNIVSLTTAESESFVLDFPQPSADY 120

Query: 122 LDPRNRLQADHVCLENCVLKDKAIAAGTVKVNLAPEKTVKIRMTFDTWKS+TDFPCQYVK 181
LDPRNRLQ +HVCLENCVLK+KAIAGTVKVNLAPEK VKIRMTFDTWKS+TDFPCQYVK
Sbjct: 121 LDPRNRLQTNHVCLENCVLKEKAIAGTVKVNLAPEKVVKIRMTFDTWKSPTDFPCQYVK 180

Query: 182 DTYAGSDRDTFSFDISLPEKIQSYERMEFAVYECNQQTWDSNRGKNYRIIRAEKSTQ 241
DTYAGSDRDTFSFDISLPEKIQSYERMEFAV YECNQ+YWDSN+GENYRI RAEK+STQ
Sbjct: 181 DTYAGSDRDTFSFDISLPEKIQSYERMEFAVCTECNQSYWDSNKGKNYRITRAELSTQ 240

Query: 242 GMTKPHSGPDGIFSFDQFGSPRCSYGLFPEWPSYLGYEKLGPHY 285
GMT+P++GPD GISFDQFGSPRCS+GLFPEWPSYLGYEKLGPHY
Sbjct: 241 GMTPEYNGPDGIFSFDQFGSPRCSFGLFPEWPSYLGYEKLGPHY 284

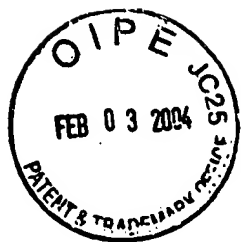
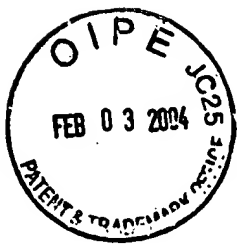


FIG. 31

CTGTCCTCGCATTCCTGAAACCTTCATCCACACAATGCCTCCCAACCTCACTGGC
TACTACCGCTTTGTCTCGCAGAAGAACATGGAGGACTACCTGCAAGCCCTAAACATC
AGCTTGGCTGTGCGGAAGATCGCGCTGCTGCTGAAGCCGGACAAGGAGATCGAACA
CCAGGGCAACCACATGACGGTGAGGACGCTCAGCACCTTCGAAACTACACTGTGC
AGTTGATGTGGGAGTGAGTTTGAGGAGGACCTCAGGAGCGTGACGGACGAAAA
TGCCAGATCTATTTCGTCGGTTCGGATCCAAGCCAGTTCTGTGGTCAGCAAGGCTCC
CCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGTTTGCGG
CTGACCTTCGCGACACAGCCTTCCTCGGAGAACAAAGACTGCCCCACCTCCACAAGGGC
TTCTGGCCCTCTACCAAACCGTGGCCTTAAGTGGAAGCTTGAGTGACAGCTGAGGC
TGGGACTCAGGGACACCTGGGCTGGATCCCAGCCCTGCC



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FIG. 32

**MPPNLTGYR FVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFR
NYTVQFDVGVEFEEDLRSVDGRKCQISFVGSDPSQFCGQQGSPLGRPPGQREFVSSGRSL
RLTFRTQPSSSENKTAHLHKGFLALYQTVALSGSLSDS**



FIG. 33

Score = 355 (125.0 bits), Expect = $1.0e-31$, P = $1.0e-31$
Identities = 68/70 (97%), Positives = 70/70 (100%), Frame = +2

Query: 38 MPPELTGTYRFFVSCQOMEDYLQALNISLAVKIALLLKPKKEIEHQGEMTVKILSTFR 217
MPPELTGTYRFFVSCQOMEDYLQALNISLAVKIALLLKPKKEIEHQGEMTVKILSTFR
Sbjct: 1 MPPELTGTYRFFVSCQOMEDYLQALNISLAVKIALLLKPKKEIEHQGEMTVKILSTFR 60

Query: 218 YTVQFDVGVE 247
YV+QFDVGVE
Sbjct: 61 YTVQFDVGVE 70



FIG. 34

CTGTCCTCTGCATTCTCCTGAAACCTTCATCCACACAATGCCTCCCAACCTCACTGGCTACTACCGCTTT
GTCTCGCAGAAGAACATGGAGGACTACCTGCAAGCCCTAAACATCAGCTTGGCTGTGCGGAAGATCGCGC
TGCTGCTGAAGCCGGACAAGGAGATCGAACACCAGGGCAACCACATGACGGTGAGGACGCTCAGCACCTT
CCGAAACTACACTGTGCAGTTTGATGTGGGAGTGGAGTTTGAGGAGGACCTCAGGAGCGTGGACGGACGA
AAATGCCAGACCATAGTAACCTGGGAGGAGGAGCACCTGGTGTGTGTGCAGAAAGGGGAGGTCCCCAACC
GGGGCTGGAGACACTGGCTGGAGGGAGAGTTGCTGTATCTGGAACTGACTGCAAGGGATGCAGTGTGCGA
GCAGGTCTTCAGGAAGGTCAGATAGCCGGAGAGGAGCCAAGATCCCTCCAGACAGCACCAGCTCACAGAC
GCTCTTGTGTGCCCCCTTCAAGCCCAGATTGTGCCAGATCTCATTCGTCGGTTCGGATCCAAGCCAGTT
CTGTGGTCAGCAAGGCTCCCCCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGT
TTGCGGCTGACCTTCCGCACACAGCCTTCCTCGGAGAAACAAGACTGCCACCTCCACAAGGGCTTCCTGG
CCCTCTACCAAACCGTGGGTGAGTGTCCCTCCTGGGGGTGCAGGGAGGGAGCCTCTGTTCACAGCCATGA
CCCTGGTATCTTCAAGCCTTAAGTGAAGCTTGAGTGACAGCTGAGG



FIG. 35

MPPNLTGYRFFVSQKNMEDYLQALNISLAVRKIALLLKPKETEHQGNHMTVRTLSTFRNYTVQFDVGVE
FEEDLRSDGRKCQTIVTWEEHLVCVQKGEVFNRGWRHWLEGELLYLELTARDAVCEQVFRKVR



FIG. 36

Score = 712 (250.6 bits), Expect = 1.5e-69, P = 1.5e-69
Identities = 133/135 (98%), Positives = 135/135 (100%), Frame =
+2

Query: 38 MPPHLTGTYRFVSQKMEYTLQALNLSLAVRKIALLLKPKKIEHQGHMTVRLSTFRN 217
MPPHLTGTYRFVSQKMEYTLQALNLSLAVRKIALLLKPKKIEHQGHMTVRLSTFRN
Sbjct: 1 MPPHLTGTYRFVSQKMEYTLQALNLSLAVRKIALLLKPKKIEHQGHMTVRLSTFRN 60

Query: 218 YTVQFDVGVFEEDLSVDGRKQQTIVTWEEHLVCVQKGEVPHRGWRHMLEGELLYLEL 397
YT+QFDVGVFEEDLSVDGRKQQTIVTWEEHLVCVQKGEVPHRGWRHMLEG+LYLEL
Sbjct: 61 YTLQFDVGVFEEDLSVDGRKQQTIVTWEEHLVCVQKGEVPHRGWRHMLEG+LYLEL 120

Query: 398 TARDVCEQVFRKVR 442
TARDVCEQVFRKVR
Sbjct: 121 TARDVCEQVFRKVR 135



FIG. 37

C018653_A MPPNLTGTVTFVSCCHHEDYLQALNLSLAVRNIALLLNFDNEIEHDEWENTVRTLSTFR
C018653_dal_ MPPNLTGTVTFVSCCHHEDYLQALNLSLAVRNIALLLNFDNEIEHDEWENTVRTLSTFR

C018653_A VVCFQNGVETEEELLSVGRNDISFVGS PSQF G QSSPLGEEQEESSRSR
C018653_dal_ VVCFQNGVETEEELLSVGRNDISFVGS PSQF G QSSPLGEEQEESSRSR

C018653_A TFRTQPSSSENKTAHLH EFLLYOTVALSDSLSD
C018653_dal_ ELTARDAVCEQVFRKV